

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 17, 2003, 09:15:23 ; Search time 1230 Seconds  
(without alignments)  
698.457 Million cell updates/sec

Title: US-10-033-243-132

Perfect score: 21

Sequence: 1 tcgtcgaacgttcgatgatc 21

Scoring table:

OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2688711 seqs, 2045481386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

GenEmbl:\*

1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
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33: em\_hcg\_mus:\*  
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37: em\_hcg\_vrt:\*  
38: em\_hcg\_hum:\*  
39: em\_hcg\_mus:\*  
40: em\_hcg\_mus:\*  
41: em\_hcg\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	6	AX592442 Sequence
2	19	90.5	19	6	AX592329 Sequence
3	19	90.5	22	6	AX592340 Sequence
4	16	76.2	18	6	AX592324 Sequence
5	16	76.2	119972	2	AP004029 Sequence
6	16	76.2	126038	8	AP000367 Sequence
7	16	76.2	144952	2	AP005629 Sequence
8	16	76.2	145668	2	AC141727 Sequence
9	16	76.2	166304	2	AC130730 Sequence
10	15	71.4	22	6	AR287741 Sequence
11	15	71.4	22	6	AR287743 Sequence
12	15	71.4	22	6	AR287743 Sequence
13	15	71.4	22	6	AR308057 Sequence
14	15	71.4	22	6	AX035945 Sequence
15	15	71.4	22	6	AX046993 Sequence
16	15	71.4	22	6	AX083675 Sequence
17	15	71.4	22	6	AX083676 Sequence
18	15	71.4	22	6	AX135650 Sequence
19	15	71.4	22	6	AX148636 Sequence
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22	15	71.4	22	6	AX250702 Sequence
23	15	71.4	22	6	AX252291 Sequence
24	15	71.4	22	6	AX252292 Sequence
25	15	71.4	22	6	AX252509 Sequence
26	15	71.4	22	6	AX252510 Sequence
27	15	71.4	22	6	AX252520 Sequence
28	15	71.4	22	6	AX252521 Sequence
29	15	71.4	22	6	AX252934 Sequence
30	15	71.4	22	6	AX252935 Sequence
31	15	71.4	22	6	AX253113 Sequence
32	15	71.4	22	6	AX253114 Sequence
33	15	71.4	22	6	AX253123 Sequence
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39	15	71.4	22	6	AX592332 Sequence
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Pred. No. is the number of results predicted by chance to have a

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## ALIGNMENTS

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RESULT 1
LOCUS AX592442 21 bp DNA linear PAT 27-JAN-2003
DEFINITION Sequence 132 from Patent WO02052002.
ACCESSION AX592442
VERSION AX592442.1 GI:27950544
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Fearon,K.L. and Dina,D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 132 04-JUL-2002;
DynaVax Technologies Corporation (US)
FEATURES
source
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/organism="synthetic construct"
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/note="Polynucleotide containing CG"
BASE COUNT 5 a 4 c 6 g 6 t
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Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCGTGAACGTTGAGATGAT 21
DB 1 TCGTGAACGTTGAGATGAT 21

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RESULT 2
LOCUS AX592329 19 bp DNA linear PAT 27-JAN-2003
DEFINITION Sequence 19 from Patent WO02052002.
ACCESSION AX592329
VERSION AX592329.1 GI:27950431
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Fearon,K.L. and Dina,D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 19 04-JUL-2002;
DynaVax Technologies Corporation (US)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCGTGAACGTTGAGATG 19
DB 1 TCGTGAACGTTGAGATG 19

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RESULT 3
LOCUS AX592340 22 bp DNA linear PAT 27-JAN-2003
DEFINITION Sequence 30 from Patent WO02052002.
ACCESSION AX592340
VERSION AX592340.1 GI:27950442
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Fearon,K.L. and Dina,D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 30 04-JUL-2002;
DynaVax Technologies Corporation (US)
FEATURES
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/note="Polynucleotide containing CG"
BASE COUNT 5 a 4 c 7 g 6 t
ORIGIN
Query Match 90.5%; Score 19; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCGTGAACGTTGAGATG 19
DB 4 TCGTGAACGTTGAGATG 22

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RESULT 4
LOCUS AX592324 18 bp DNA linear PAT 27-JAN-2003
DEFINITION Sequence 14 from Patent WO02052002.
ACCESSION AX592324
VERSION AX592324.1 GI:27950426
KEYWORDS

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SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Fearon, K.L. and Dina, D.  
TITLE Immunomodulatory polynucleotides and methods of using the same  
JOURNAL Patent: WO 02052002-A 14 04-JUL-2002;  
Dynavax Technologies Corporation (US)  
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SOURCE  
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/note="Polynucleotide containing CG"

BASE COUNT 4 a 4 c 5 g 5 t  
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 21;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 TCGAACGTTCCGATG 19  
Db 3 TCGAACGTTCCGATG 18

RESULT 5  
AP004029 119972 bp DNA linear HTG 21-MAR-2002  
LOCUS Oryza sativa (japonica cultivar-group) chromosome 2 clone  
DEFINITION OJ1136 D07, \*\*\* SEQUENCING IN PROGRESS \*\*\*.  
AP004029  
VERSION AP004029.1 GI:15130691  
KEYWORDS HTG; HTGS\_PHASE2.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE 1  
AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.  
TITLE Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, BAC  
clone:OJ1136 D07  
JOURNAL Published Only in Database (2001)  
AUTHORS 2 (bases 1 to 119972)  
Sasaki, T., Matsumoto, T. and Yamamoto, K.  
TITLE Direct Submission  
JOURNAL Submitted (08-AUG-2001) Takuji Sasaki, National Institute of  
Agrobiological Resources, Rice Genome Research Program; Kamondai  
2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,  
Tel:81-298-38-7441, Fax:81-298-38-7468)  
COMMENT The nucleotide sequence of this BAC clone was generated by  
combining Monsanto and RGP-Japan sequencing data.  
NOTE: It currently consists of 1 contigs. Gaps between the contigs  
are represented as runs of N. The order of the pieces is believed  
to be correct as given, however the sizes of the gaps between them  
are based on estimates that have provided by the submitter. This  
sequence will be replaced by the finished sequence as soon as it is  
available and the accession number will be preserved.  
\* NOTE: This is a 'working draft' sequence.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
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/mol\_type="genomic DNA"  
/cultivar="Nipponbare"  
/db\_xref="taxon:39947"  
/chromosome="2"  
/clone="OJ1136 D07"  
BASE COUNT 34735 a 25005 c 25414 g 34818 t

ORIGIN

Query Match 76.2%; Score 16; DB 2; Length 119972;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 CGAACGTTCCGATG 20  
Db 38384 CGAACGTTCCGATG 38399

RESULT 6  
AP000367 126038 bp DNA linear PLN 21-MAR-2002  
LOCUS Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2,  
DEFINITION clone:PO437H03 (contig b).  
AP000367  
VERSION AP000367.1 GI:5441876  
KEYWORDS  
SOURCE  
ORGANISM Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE 1  
AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.  
TITLE Oryza sativa Nipponbare (GA3) genomic DNA, chromosome 2, PAC  
clone:PO437H03 (contig b)  
JOURNAL Published Only in Database (1999)  
AUTHORS 2 (bases 1 to 126038)  
Sasaki, T., Matsumoto, T. and Yamamoto, K.  
TITLE Direct Submission  
JOURNAL Submitted (06-JUL-1999) Takuji Sasaki, National Institute of  
Agrobiological Resources, Rice Genome Research Program; Kamondai  
2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,  
Tel:81-298-38-7441, Fax:81-298-38-7468)  
COMMENT This PAC clone has 10 kbp sequence gap, which result in 2 contigs  
(contig a, b). This sequence shows contig b. The orientation of the  
sequence is from S86 to T7 of the PAC clone. Genes were predicted  
from the integrated results of the following:GENSCAN1.0, BLASTN1.4,  
BLASTX2.0 as well as SplicePredictor (October1998 version). The  
genomic sequence was searched against the non-redundant database  
NR(PfR, SWISSPROT, GENEPIR, PDB) from MAF DMBank and the cDNA  
sequence database at RGP. Protein similarities of the coding  
regions were searched against NRP with BLASTP2.0. ESTs represent  
the identified cDNA sequences using BLASTN1.4 with the  
corresponding DBJ accession no. and RGP clone ID.  
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/db\_xref="taxon:39947"  
/chromosome="2"  
/clone="PO437H03 (contig b)"  
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2428..2541,2732..2868,3006..3116,5410..5554)) (BC  
2.4.1.186). (297341)"  
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KRDFTVEDMDIARSLGKMKFVYLQGVSELSFPAKRFPOHRSVSNVDEGVM  
MLMEIVRKVYTIWKIHYVFLIRIKIHYIYFAPYCAIIPATIEVPEVRILPKG  
CVYIPITILNSVGTSPRFLILFEMILFEWVMSLHRKATLIGLEGRANVWVTE  
KLGNAUKKSSSKSASAKSPFRVWDRNLNVTLSGAAPLPSGGMWDLARGDHFIYLR  
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13319..13331)  
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Similar to Arabidopsis thaliana BAC genomic sequence.  
(AC002292)"  
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19855..20113,20190..20488,21053..21389,21495..21645,  
22169..22484,22743..22774,23219..24224))  
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Similar to maize transposon Mudra mudra protein.  
(AC003981)"  
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SSVGNICPEBKSTIRHLENKKTITSYAKAMRAOKITIMRYGTFEASYNPLULA  
TYQKNNNTYDHLHTFISVDDRTKSVLDGAFSLGACINAFHCPVLCIDGETYTGK  
YRGQLTAIGCGNNQVLPMAFAVESNTESWYLFVHVAVCKMPNCLHDIRH  
AEVNMVWGVCEVLKADGCTCSCKMPKHLHPCSHVLAAGCGISPMVYNSYF  
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PYDVGFMKEDITAFKEOVWRLPHLGPTTLTPPSTVSGSKAWLQFRRKRAVAVR  
GYPDFVFEFDRLOPSDVIWEPTYEAVARAVALGSLCTRQAWMLTILPVPDIFV  
EPHCPQVWROGLROVPFGVNPVLPADHSLTRQGLAGLMAFPAVQOYVDVLA  
TEEVNELFPHTEENYRDLYRWLYPRTARVFTPDAPFHYAAVTDAYPFRHDFY  
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SPGTYQKNAHTTIDTGVETTYFIANTLYQGLSTCOLIAONPLHDSRGVAGDNL  
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VSGDVGEGVILKRVNHCSLIRLSGLCVHRGDTVVEPYAENGALSDMLHGDGDAATQ  
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AGDGAALAAQOTRHVGTQGLSPEYIEHLITPKLDPAFAGVALLLSLGEKVAAS  
GDGENGALILMESAAELVDGGEDAGSNRAFMFDPRLGIDYPLDILMAVAASLAARC  
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LAVASALAAVKAAPRRRGARGGDRKKVTRVTPRDEBLDGDVILLHEKKNERTIG  
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VSELERTIDLRVOTTYNIRVYFLANRPPAPRNGCAAAAACACACGCGLLD  
VAFPCISGCKLKCHESDPTITFTIDPNKITEFQISGPEDEEDDEDFPTTKA  
NAAOSKAGGGGCGPPEPPSASSRPRRGVAVRGKEDEQEAANILAPAAAAAS  
VPASADPNSYRRARRGARAPERSFPF"  
join(55812..55816,55861..55978,56109..56216,56457..56732,  
57319..57365,57427..57778)  
/note="EST AU069246(C53478) corresponds to a region of the  
predicted gene.  
hypothetical protein"  
/codon\_start=1  
/protein\_id="BAA82384.1"  
/db\_xref="GI:5441886"  
/translation="WRVQLFTHHAREILIRHRTYRTLQWRILSHYDTRHCTG  
NVQSTTHAHTCPVLNVACTIPGKRRTYVHVSIVTWSSSSSSSPARSPTAA  
TPDRRRSGSPARAGECDKGVVEYRKEEISPRIVSSAPRAAATSGGAALR  
OSRGEGILGVTGNAAPKRYATSOIABEELARREVLPTSGTKAKAPKTFPKNEP  
HSAPOSDMGTPDSVBERGPADEYALRKVYLLDENGEIDLKQLSQAEBSAVLEDEK  
FALDOLVYLEGVDPSCMOBPRRL"  
join(58631..58875,59008..59067,59212..59356,59467..59628)  
/note="Similar to Arabidopsis thaliana BAC genomic  
sequence. (AC002332)"  
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/db\_xref="GI:5441887"  
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FKEVNRFPKRRNNVGLNRLKALVADPAQALALAAARKMEALDEYSGEDLPWID  
CKINVOSEFPKRGCGSLVYIEBCVAFWMDRKYKIDRLYKWLVEYAGNCSSEVI  
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Query Match 76.2%; Score 16; DB 8; Length 126038;  
Best Local Similarity 100.0%; Pred. NO. 25;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 CGAAGTTTCGAGATGA 20



Db 27299 CGAAGCTTCGAGATGA 27284

RESULT 7  
AP005629

LOCUS

DEFINITION AP005629 144952 bp DNA linear HTG 08-AUG-2002  
OSJNB00004A19, \*\*\* SEQUENCING IN PROGRESS \*\*\*.

ACCESSION AP005629

VERSION AP005629.1 GI:22138853

KEYWORDS HTG; HTGS PHASE2.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Erihartoideae; Oryzaceae; Oryza.

REFERENCE 1  
Sasaki, T., Matsumoto, T. and Katayose, Y.  
Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, BAC  
clone: OSJNB0004A19  
Published Only in Database (2002)

JOURNAL 2 (bases 1 to 144952)

REFERENCE Sasaki, T., Matsumoto, T. and Katayose, Y.  
Agricultural Sciences, Rice Genome Research Program, Kamondai  
2-1-2, Takubaba, Ibaraki 305-8602, Japan  
(E-mail: tsasaki@affrc.affrc.go.jp, URL: http://rsgp.dna.affrc.go.jp/  
Tel: 81-298-38-7441, Fax: 81-298-38-7468)

AUTHORS NOTE: It currently consists of 1 contigs. Gaps between the contigs  
are represented as runs of N. The order of the pieces is believed  
to be correct as given, however the sizes of the gaps between them  
are based on estimates that have provided by the submitter. This  
sequence will be replaced by the finished sequence as soon as it is  
available and the accession number will be preserved.

TITLE \* NOTE: This is a 'working draft' sequence.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.

FEATURES  
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/mol\_type="genomic DNA"  
/cultiivar="Nipponbare"  
/db\_xref="taxon:39947"  
/chromosome="2"  
/clone="OSJNB0004A19"

BASE COUNT 41769 a 30336 c 30932 g 41813 t 102 others

ORIGIN

Query Match 76.2%; Score 16; DB 2; Length 144952;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGCTTCGAGATGA 20  
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Db 33857 CGAAGCTTCGAGATGA 33872

RESULT 8  
AC141727/c

LOCUS AC141727 146568 bp DNA linear HTG 19-MAR-2003

DEFINITION Apis mellifera clone CH224-57G3, WORKING DRAFT SEQUENCE, 25  
unordered pieces.

ACCESSION AC141727

VERSION AC141727.1 GI:29123911

KEYWORDS HTG; HTGS PHASE1; HTGS\_DRAFT.

SOURCE Apis mellifera (honeybee)

ORGANISM Apis mellifera  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;  
Apidae; Apis.

REFERENCE 1 (bases 1 to 146568)

AUTHORS Mizny, D.M., Adams, C., Adio-Oduola, B., Ali-Usman, F.R., Allen, C.,  
Alshrocks, S.L., Amaratunga, H.C., Are, J.R., Ayele, M., Banks, T.,  
Barbata, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,  
Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,  
Buhay, C., Burck, P., Burkett, C., Burrell, K.L., Byrd, N.C.,  
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,  
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,  
Cleveland, C.D., Cox, C., Coyle, M.D., Dahorne, S.R., David, R.,  
Davis, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,  
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,  
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,  
Eamhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotro, M.,  
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,  
Gabisi, A., Geo, J., Garcia, A., Garner, T., Garza, N., Gill, R.,  
Gorrell, J.H., Guevara, M., Gunatane, P., Hale, S., Hamilton, K.,  
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,  
Hernandez, O., Hodgson, A., Hognes, M., Holloway, C., Hollins, B.,  
Homes, F., Howard, S., Huber, J., Hulvik, S., Hume, J., Jackson, L.E.,  
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,  
Karlsom, E., Kelly, S., Khan, U., King, L., Korvah, J., Kover, C.,  
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,  
Li, J., Li, Z., Licharge, O., Lieu, C., Liu, J., Liu, W., Louised, H.,  
Lozad, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,  
Maheshwari, M., Mapa, P., Martin, R., Martindale, A., Martinez, E.,  
Massey, E., Mawhinney, E., McLeod, M.P., Meador, K., Morgan, M., Morris, S.,  
Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S.,  
Moser, M., Neal, D., Newcomb, J., Newton, S., Nguyen, A., Nguyen, N.,  
Nguyen, N., Nickerson, E., Nwokenwo, S., Ogund, M., Okunodu, G.,  
Oreguine, N., Oviado, R., Pace, A., Payton, B., Peery, J., Perez, J.,  
Peterson, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,  
Rivers, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G.,  
Scherrer, S., Scott, G., Shen, H., Shoohtari, N., Sisson, I.,  
Sodergren, E., Sonake, T., Sparks, A., Stanley, H., Stone, H.,  
Sutton, A., Swatek, A., Taber, P., Tameris, K., Tang, H.,  
Tansley, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,  
Uman, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q.,  
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watling, S.,  
Williams, G., Williamson, A., Wlezyk, R., Wooten, S., Worley, K.,  
Wu, C., Wu, Y., Wu, Y.F., Zhou, D., Zorrilla, S., Nelson, D.,  
Weinstock, G. and Gibbs, R.

TITLE Unpublished

JOURNAL 2 (bases 1 to 146568)

REFERENCE Worley, K.C.

AUTHORS Direct Submission

TITLE Submitted (19-MAR-2003) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

JOURNAL

COMMENT

Center: Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/  
Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: AMEZ

Center clone name: CH224-57G3

Summary Statistics

Sequencing vector: Plasmid

Chemistry: Dye-terminator Big Dye 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 132495 bases at least Q40

Consensus quality: 137202 bases at least Q30

Consensus quality: 140042 bases at least Q20

Estimated insert size: 137866; sum-of-contigs estimation

Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length  
(see http://www.hgsc.bcm.tmc.edu/docs/genbank\_draft\_data.html).  
NOTE: This is a 'working draft' sequence. It currently  
consists of 25 contigs. The true order of the pieces  
is not known and their order in this sequence record is  
arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1456: contig of 1456 bp in length  
\* 1557 1556: gap of unknown length  
\* 2732 2731: contig of 1175 bp in length  
\* 2832 2831: gap of unknown length  
\* 4180 4180: contig of 1349 bp in length  
\* 4281 4280: gap of unknown length  
\* 5835 5835: contig of 1555 bp in length  
\* 5936 5935: gap of unknown length  
\* 7358 7358: contig of 1423 bp in length  
\* 7459 7458: gap of unknown length  
\* 8917 8916: gap of 1358 bp in length  
\* 10937 10936: contig of 2020 bp in length  
\* 11037 11036: gap of unknown length  
\* 12382 12381: contig of 1345 bp in length  
\* 1482 1481: gap of unknown length  
\* 15062 15062: contig of 2581 bp in length  
\* 15162 15162: gap of unknown length  
\* 18933 18933: contig of 3771 bp in length  
\* 18934 18933: gap of unknown length  
\* 19034 19033: gap of unknown length  
\* 22107 22106: contig of 4073 bp in length  
\* 23207 23206: gap of unknown length  
\* 27707 27707: contig of 4501 bp in length  
\* 27808 27807: gap of unknown length  
\* 33059 33059: contig of 5252 bp in length  
\* 33160 33159: gap of unknown length  
\* 38669 38669: contig of 5510 bp in length  
\* 38670 38669: gap of unknown length  
\* 38770 38769: gap of unknown length  
\* 45436 45436: contig of 6667 bp in length  
\* 45536 45536: gap of unknown length  
\* 52247 52247: contig of 6711 bp in length  
\* 52348 52347: gap of unknown length  
\* 52348 52347: gap of unknown length  
\* 59244 59244: contig of 6897 bp in length  
\* 59245 59244: gap of unknown length  
\* 59345 59344: gap of unknown length  
\* 66497 66497: contig of 7153 bp in length  
\* 66598 66597: gap of unknown length  
\* 74127 74127: contig of 7530 bp in length  
\* 74128 74127: gap of unknown length  
\* 74228 74227: gap of unknown length  
\* 81723 81722: contig of 7495 bp in length  
\* 81823 81822: gap of unknown length  
\* 92875 92875: contig of 11053 bp in length  
\* 92876 92875: gap of unknown length  
\* 101243 101243: contig of 8268 bp in length  
\* 101244 101243: gap of unknown length  
\* 101344 101343: contig of 12526 bp in length  
\* 113870 113869: gap of unknown length  
\* 113970 113969: gap of unknown length  
\* 128447 128447: contig of 14478 bp in length  
\* 128448 128447: gap of unknown length  
\* 128548 128547: gap of unknown length  
\* 146568 146568: contig of 18021 bp in length.

FEATURES  
source 1. 146568  
Location/Qualifiers  
/organism="Apis mellifera"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7460"  
/clone="CH224-57G3"

BASE COUNT 39316 a 30537 c 30943 g 39489 t 6283 others

ORIGIN  
Query Match 76.2%; Score 16; DB 2; Length 146568;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGTCGACGTTGAGA 17  
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Db 135270 CGTCGACGTTGAGA 135255

RESULT 9  
AC130730/c

LOCUS AC130730 166304 bp DNA linear HTG 14-AUG-2002  
DEFINITION Oryza sativa (japonica cultivar-group) chromosome 5 clone P0681D04,  
\*\*\* SEQUENCING IN PROGRESS \*\*\*; 6 ordered pieces.

ACCESSION AC130730  
VERSION AC130730.1 GI:22218364  
KEYWORDS HTG; HTGS PHASE2.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Euphorbiales; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Euphorbiaceae; Oryzae; Oryza.  
1 (bases 1 to 166304)  
Chow, T.-Y., Hsing, Y.-I. C., Chen, C.-S., Chen, H.-H., Liu, S.-M.,  
Chen, Y.-I., Chang, S.-J., Chen, H.-C., Chen, S.-K., Chen, T.-R.,  
Chen, Y.-L., Cheng, C.-H., Chung, C.-I., Han, S.-Y., Hsiao, S.-H.,  
Hsiao, J.-N., Hsu, C.-H., Huang, J.-J., Kau, P.-I., Lee, M.-C.,  
Lien, H.-L., Li, Y.-F., Lin, S.-J., Lin, Y.-C., Wu, S.-W., Yu, C.-Y.,  
Yu, S.-W., Wu, H.-P., and Shaw, J.-F.  
Oryza sativa PAC P0681D04 genomic sequence

TITLE Oryza sativa PAC P0681D04 genomic sequence  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 166304)  
Chow, T.-Y., and Hsing, Y.-I. C.  
AUTHORS Direct Submission  
JOURNAL Submitted (14-AUG-2002) Institute of Botany, Academia Sinica, 128,  
Section 2, Academia Road, Nankang, Taipei 11529, Taiwan

COMMENT  
\* NOTE: This is a working draft sequence. It currently  
\* consists of 6 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.

1 8678: contig of 8678 bp in length  
\* 8679 8678: gap of unknown length  
\* 8779 8778: gap of unknown length  
\* 14903 14903: contig of 6125 bp in length  
\* 14904 14903: gap of unknown length  
\* 15004 15003: contig of 20390 bp in length  
\* 35393 35393: gap of unknown length  
\* 35494 35493: gap of unknown length  
\* 121325 121324: contig of 85831 bp in length  
\* 121425 121424: gap of unknown length  
\* 121425 121424: gap of unknown length  
\* 135357 135356: contig of 13932 bp in length  
\* 135357 135356: gap of unknown length  
\* 135457 135456: gap of unknown length  
\* 166304 166304: contig of 30848 bp in length.

FEATURES  
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Location/Qualifiers  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="genomic DNA"  
/cultivar="Nipponbare"  
/db\_xref="taxon:39947"  
/chromosome="5"  
/clone="P0681D04"

BASE COUNT 46182 a 37272 c 36481 g 45869 t 500 others

ORIGIN  
Query Match 76.2%; Score 16; DB 2; Length 166304;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACGTTGAGATCA 20  
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Db 99712 CGACGTTGAGATCA 99697

RESULT 10  
AR268334 22 bp DNA linear PAT 10-APR-2003  
LOCUS AR268334  
DEFINITION Sequence 19 from patent US 6498148.  
ACCESSION AR268334  
VERSION AR268334.1 GI:29698684  
KEYWORDS Unknown.  
SOURCE

ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Raz,E.  
TITLE Immunization-free methods for treating antigen-stimulated inflammation in a mammalian host and shifting the host's antigen immune responsiveness to a Th1 phenotype  
JOURNAL Patent: US 6498148-A 19 24-DEC-2002;  
FEATURES location/Qualifiers  
source 1..22  
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BASE COUNT 6 a 3 c 7 g 6 t  
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
8 GAACGTCGAGATGA 22

Db

RESULT 11  
LOCUS AR287741 22 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 1 from patent US 6534062.  
ACCESSION AR287741  
VERSION AR287741.1 GI:31674761  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Raz,E., Cho,H.J., Richman,D. and Horner,A.A.  
TITLE Methods for increasing a cytotoxic T lymphocyte response in vivo  
JOURNAL Patent: US 6534062-A 1 18-MAR-2003;  
FEATURES location/Qualifiers  
source 1..22  
/organism="unknown"  
BASE COUNT 6 a 3 c 7 g 6 t  
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
8 GAACGTCGAGATGA 22

Db

RESULT 12  
LOCUS AR287743 22 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 3 from patent US 6534062.  
ACCESSION AR287743  
VERSION AR287743.1 GI:31674763  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Raz,E., Cho,H.J., Richman,D. and Horner,A.A.  
TITLE Methods for increasing a cytotoxic T lymphocyte response in vivo  
JOURNAL Patent: US 6534062-A 3 18-MAR-2003;  
FEATURES location/Qualifiers  
source 1..22  
/organism="unknown"  
BASE COUNT 6 a 3 c 7 g 6 t  
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
8 GAACGTCGAGATGA 22

Db

RESULT 13  
LOCUS AR308057 22 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 1 from patent US 6552006.  
ACCESSION AR308057  
VERSION AR308057.1 GI:31698950  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Raz,E., Kornbluth,R., Catanzaro,A., Hayashi,T. and Carson,D.  
TITLE Immunomodulatory polynucleotides in treatment of an infection by an intracellular pathogen  
JOURNAL Patent: US 6552006-A 1 22-APR-2003;  
FEATURES location/Qualifiers  
source 1..22  
/organism="unknown"  
BASE COUNT 6 a 3 c 7 g 6 t  
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
8 GAACGTCGAGATGA 22

Db

RESULT 14  
LOCUS AX036945 22 bp DNA linear PAT 16-NOV-2000  
DEFINITION Sequence 2 from Patent FR2790955.  
ACCESSION AX036945  
VERSION AX036945.1 GI:11226373  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1  
AUTHORS Carpentier,A.  
JOURNAL Patent: FR 2790955-A 2 22-SEP-2000;  
ASSIST PUBL HOPITAUX DE PARIS (FR)  
FEATURES location/Qualifiers  
source 1..22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Oligodeoxynucleotide"  
BASE COUNT 6 a 3 c 7 g 6 t  
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
8 GAACGTCGAGATGA 22

Db

RESULT 15  
LOCUS AX046993 22 bp DNA linear PAT 15-DEC-2000  
AX046993

DEFINITION Sequence 2 from Patent WO0067787.  
ACCESSION AX046993  
VERSION AX046993.1 GI:11876420  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
artificial sequences.  
REFERENCE  
1  
AUTHORS  
TITLE  
JOURNAL  
Moss, R.B.  
Hiv immunogenic compositions and methods  
Patent: WO 0067787-A 2 16-NOV-2000;  
THE IMMUNE RESPONSE CORPORATION (US)  
FEATURES  
source  
1..22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="phosphorothioate-modified synthetic  
oligodeoxynucleotide"  
BASE COUNT 6 a 3 c 7 g 6 t  
ORIGIN  
Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTCGAGATGA 20  
|||||  
Db 8 GAACGTCGAGATGA 22

RESULT 16  
AX083675 22 bp DNA linear PAT 28-FEB-2001  
LOCUS  
DEFINITION Sequence 1 from Patent WO0112223.  
ACCESSION AX083675  
VERSION AX083675.1 GI:13185407  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
artificial sequences.  
REFERENCE  
1  
AUTHORS  
TITLE  
JOURNAL  
van Nest, G.  
Methods of modulating an immune response using immunostimulatory s  
equences and compositions for use therein  
Patent: WO 0112223-A 1 22-FEB-2001;  
Dynavax Technologies Corporation (US)  
FEATURES  
source  
1..22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic construct"  
BASE COUNT 6 a 3 c 7 g 6 t  
ORIGIN  
Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTCGAGATGA 20  
|||||  
Db 8 GAACGTCGAGATGA 22

RESULT 17  
AX083676 22 bp DNA linear PAT 28-FEB-2001  
LOCUS  
DEFINITION Sequence 2 from Patent WO0112223.  
ACCESSION AX083676  
VERSION AX083676.1 GI:13185408  
KEYWORDS  
SOURCE  
synthetic construct

ORGANISM  
synthetic construct  
artificial sequences.  
REFERENCE  
1  
AUTHORS  
TITLE  
JOURNAL  
van Nest, G.  
Methods of modulating an immune response using immunostimulatory s  
equences and compositions for use therein  
Patent: WO 0112223-A 2 22-FEB-2001;  
Dynavax Technologies Corporation (US)  
FEATURES  
source  
1..22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic construct"  
BASE COUNT 6 a 4 c 7 g 5 t  
ORIGIN  
Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTCGAGATGA 20  
|||||  
Db 8 GAACGTCGAGATGA 22

RESULT 18  
AX135650 22 bp DNA linear PAT 29-MAY-2001  
LOCUS  
DEFINITION Sequence 21 from Patent WO0132877.  
ACCESSION AX135650  
VERSION AX135650.1 GI:14271920  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
artificial sequences.  
REFERENCE  
1  
AUTHORS  
TITLE  
JOURNAL  
Mackichan, M.L.  
Cpg receptor (cpg-r) and methods relating thereto  
Patent: WO 0132877-A 21 10-MAY-2001;  
CHIRON CORPORATION (US)  
FEATURES  
source  
1..22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Cpg oligonucleotide"  
BASE COUNT 6 a 3 c 7 g 6 t  
ORIGIN  
Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTCGAGATGA 20  
|||||  
Db 8 GAACGTCGAGATGA 22

RESULT 19  
AX148636 22 bp DNA linear PAT 08-JUN-2001  
LOCUS  
DEFINITION Sequence 1 from Patent WO0135991.  
ACCESSION AX148636  
VERSION AX148636.1 GI:14347254  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
synthetic construct  
artificial sequences.  
REFERENCE  
1  
AUTHORS  
TITLE  
Tuck, S. and van Nest, G.  
Immunomodulatory compositions containing an immunostimulatory  
sequence linked to antigen and methods of use thereof

JOURNAL Patent: WO 0135991-A 1 25-MAY-2001;  
Dynavax Technologies Corporation (US)  
FEATURES  
source  
1. .22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="synthetic construct"  
BASE COUNT 6 a 3 c 7 g 6 t  
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTCGAGATGA 20  
Db 8 GAACGTCGAGATGA 22

RESULT 20  
LOCUS AX148637 22 bp DNA linear PAT 08-JUN-2001  
DEFINITION Sequence 2 from Patent WO0135991.  
ACCESSION AX148637  
VERSION AX148637.1 GI:14347255  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Tuck,S. and van Nest,G.  
TITLE Immunomodulatory compositions containing an immunostimulatory  
JOURNAL Patent: WO 0135991-A 2 25-MAY-2001;  
FEATURES  
source  
1. .22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="synthetic construct"  
BASE COUNT 6 a 4 c 7 g 5 t  
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTCGAGATGA 20  
Db 8 GAACGTCGAGATGA 22

RESULT 21  
LOCUS AX250701 22 bp DNA linear PAT 06-OCT-2001  
DEFINITION Sequence 1 from Patent WO0168078.  
ACCESSION AX250701  
VERSION AX250701.1 GI:15984439  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS van Nest,G.  
TITLE Method of suppressing hepatitis virus infection using  
JOURNAL immunomodulatory polynucleotide sequences  
Patent: WO 0168078-A 1 20-SEP-2001;  
FEATURES  
source  
1. .22  
/organism="synthetic construct"  
/db\_xref="taxon:32630"

BASE COUNT 6 a 3 c 7 g 6 t  
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTCGAGATGA 20  
Db 8 GAACGTCGAGATGA 22

RESULT 22  
LOCUS AX250702 22 bp DNA linear PAT 05-OCT-2001  
DEFINITION Sequence 2 from Patent WO0168078.  
ACCESSION AX250702  
VERSION AX250702.1 GI:15984440  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS van Nest,G.  
TITLE Methods of suppressing hepatitis virus infection using  
JOURNAL immunomodulatory polynucleotide sequences  
Patent: WO 0168078-A 2 20-SEP-2001;  
FEATURES  
source  
1. .22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
BASE COUNT 6 a 4 c 7 g 5 t  
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTCGAGATGA 20  
Db 8 GAACGTCGAGATGA 22

RESULT 23  
LOCUS AX252291 22 bp DNA linear PAT 05-OCT-2001  
DEFINITION Sequence 1 from Patent WO0168117.  
ACCESSION AX252291  
VERSION AX252291.1 GI:15985632  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS van Nest,G.  
TITLE Methods of reducing papillomavirus infection using immunomodulatory  
JOURNAL polynucleotide sequences  
Patent: WO 0168117-A 1 20-SEP-2001;  
FEATURES  
source  
1. .22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"  
BASE COUNT 6 a 3 c 7 g 6 t  
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;

Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
|||||  
8 GAACGTCGAGATGA 22

RESULT 24  
AX252292 22 bp DNA linear PAT 05-OCT-2001  
LOCUS Sequence 2 from Patent WO0168117.

ACCESSION AX252292  
VERSION AX252292.1 GI:15985633  
KEYWORDS

SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 artificial sequences.

AUTHORS van Nest,G.  
TITLE Methods of reducing papillomavirus infection using immunomodulatory  
JOURNAL polynucleotide sequences  
PATENT: WO 0168117-A 2 20-SEP-2001;  
DynaVax Technologies Corporation (US)

FEATURES  
source 1..22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"

BASE COUNT 6 a 4 c 7 g 5 t  
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
|||||  
8 GAACGTCGAGATGA 22

RESULT 25  
AX252509 22 bp DNA linear PAT 05-OCT-2001  
LOCUS Sequence 1 from Patent WO0168103.

ACCESSION AX252509  
VERSION AX252509.1 GI:15985780  
KEYWORDS

SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 artificial sequences.

AUTHORS van Nest,G.  
TITLE Methods of ameliorating symptoms of herpes infection using  
JOURNAL immunomodulatory polynucleotide sequences  
PATENT: WO 0168103-A 1 20-SEP-2001;  
DynaVax Technologies Corporation (US)

FEATURES  
source 1..22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"

BASE COUNT 6 a 3 c 7 g 6 t  
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
|||||  
8 GAACGTCGAGATGA 22

DB 8 GAACGTCGAGATGA 22

RESULT 26  
AX252510 22 bp DNA linear PAT 05-OCT-2001  
LOCUS Sequence 2 from Patent WO0168103.

ACCESSION AX252510  
VERSION AX252510.1 GI:15985781  
KEYWORDS

SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 artificial sequences.

AUTHORS van Nest,G.  
TITLE Methods of ameliorating symptoms of herpes infection using  
JOURNAL immunomodulatory polynucleotide sequences  
PATENT: WO 0168103-A 2 20-SEP-2001;  
DynaVax Technologies Corporation (US)

FEATURES  
source 1..22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"

BASE COUNT 6 a 4 c 7 g 5 t  
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
|||||  
8 GAACGTCGAGATGA 22

RESULT 27  
AX252520 22 bp DNA linear PAT 05-OCT-2001  
LOCUS Sequence 1 from Patent WO0168144.

ACCESSION AX252520  
VERSION AX252520.1 GI:15985791  
KEYWORDS

SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 artificial sequences.

AUTHORS van Nest,G. and Tuck,S.  
TITLE Biodegradable immunomodulatory formulations and methods for use  
JOURNAL thereof  
PATENT: WO 0168144-A 1 20-SEP-2001;  
DynaVax Technologies Corporation (US)

FEATURES  
source 1..22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"

BASE COUNT 6 a 3 c 7 g 6 t  
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
|||||  
8 GAACGTCGAGATGA 22

RESULT 28  
AX252521

LOCUS AX252931 22 bp DNA linear PAT 05-OCT-2001  
DEFINITION Sequence 2 from Patent WO0168144.  
ACCESSION AX252931  
VERSION AX252931.1 GI:15985792  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1  
AUTHORS van Nest,G. and Tuck,S.  
TITLE Biodegradable immunomodulatory formulations and methods for use thereof  
JOURNAL Patent: WO 0168144-A 2 20-SEP-2001;  
DYNavax Technologies Corporation (US)  
FEATURES  
source  
1..22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"  
BASE COUNT 6 a 4 c 7 g 5 t  
ORIGIN  
Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 6 GAACGTCGAGATGA 20  
DB 8 GAACGTCGAGATGA 22  
RESULT 29  
LOCUS AX252934 22 bp DNA linear PAT 05-OCT-2001  
DEFINITION Sequence 1 from Patent WO0168143.  
ACCESSION AX252934  
VERSION AX252934.1 GI:15986201  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1  
AUTHORS van Nest,G. and Tuck,S.  
TITLE Immunomodulatory formulations and methods for use thereof  
JOURNAL Patent: WO 0168143-A 1 20-SEP-2001;  
DYNavax Technologies Corporation (US)  
FEATURES  
source  
1..22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"  
BASE COUNT 6 a 3 c 7 g 6 t  
ORIGIN  
Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 6 GAACGTCGAGATGA 20  
DB 8 GAACGTCGAGATGA 22  
RESULT 30  
LOCUS AX252935 22 bp DNA linear PAT 05-OCT-2001  
DEFINITION Sequence 2 from Patent WO0168143.  
ACCESSION AX252935  
VERSION AX252935.1 GI:15986202  
KEYWORDS  
SOURCE  
synthetic construct

ORGANISM  
synthetic construct  
artificial sequences.  
REFERENCE  
1  
AUTHORS van Nest,G. and Tuck,S.  
TITLE Immunomodulatory formulations and methods for use thereof  
JOURNAL Patent: WO 0168143-A 2 20-SEP-2001;  
DYNavax Technologies Corporation (US)  
FEATURES  
source  
1..22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"  
BASE COUNT 6 a 4 c 7 g 5 t  
ORIGIN  
Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 6 GAACGTCGAGATGA 20  
DB 8 GAACGTCGAGATGA 22  
RESULT 31  
LOCUS AX253113 22 bp DNA linear PAT 05-OCT-2001  
DEFINITION Sequence 1 from Patent WO0168116.  
ACCESSION AX253113  
VERSION AX253113.1 GI:15986281  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1  
AUTHORS van Nest,G.  
TITLE Methods of preventing and treating respiratory viral infection usi  
ng immunomodulatory polynucleotide sequences  
JOURNAL Patent: WO 0168116-A 1 20-SEP-2001;  
DYNavax Technologies Corporation (US)  
FEATURES  
source  
1..22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"  
BASE COUNT 6 a 3 c 7 g 6 t  
ORIGIN  
Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 6 GAACGTCGAGATGA 20  
DB 8 GAACGTCGAGATGA 22  
RESULT 32  
LOCUS AX253114 22 bp DNA linear PAT 05-OCT-2001  
DEFINITION Sequence 2 from Patent WO0168116.  
ACCESSION AX253114  
VERSION AX253114.1 GI:15986282  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1  
AUTHORS van Nest,G.  
TITLE Methods of preventing and treating respiratory viral infection usi  
ng immunomodulatory polynucleotide sequences



JOURNAL Patent: WO 0168116-A 2 20-SEP-2001;  
DynaVax Technologies Corporation (US)  
FEATURES  
source  
1. .22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"

BASE COUNT 6 a 4 c 7 g 5 t

ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGCAGATGA 20  
|||||  
8 GAACGTTGCAGATGA 22

RESULT 33  
AX253123 22 bp DNA linear PAT 05-OCT-2001  
LOCUS Sequence 1 from Patent WO0168077.  
ACCESSION AX253123  
VERSION AX253123.1 GI:15986291  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS van Nest, G.  
TITLE Methods of preventing and treating viral infections using immunomodulatory polynucleotide sequences  
JOURNAL Patent: WO 0168077-A 1 20-SEP-2001;  
DynaVax Technologies Corporation (US)  
FEATURES  
source  
1. .22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"

BASE COUNT 6 a 3 c 7 g 6 t

ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGCAGATGA 20  
|||||  
8 GAACGTTGCAGATGA 22

RESULT 34  
AX253124 22 bp DNA linear PAT 05-OCT-2001  
LOCUS Sequence 2 from Patent WO0168077.  
ACCESSION AX253124  
VERSION AX253124.1 GI:15986292  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS van Nest, G.  
TITLE Methods of preventing and treating viral infections using immunomodulatory polynucleotide sequences  
JOURNAL Patent: WO 0168077-A 2 20-SEP-2001;  
DynaVax Technologies Corporation (US)  
FEATURES  
source  
1. .22  
/organism="synthetic construct"

/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"

BASE COUNT 6 a 4 c 7 g 5 t

ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGCAGATGA 20  
|||||  
8 GAACGTTGCAGATGA 22

RESULT 35  
AX468499 22 bp DNA linear PAT 16-JUL-2002  
LOCUS Sequence 19 from Patent WO0226209.  
ACCESSION AX468499  
VERSION AX468499.1 GI:21901329  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS O'Hagan, D., Otten, G., Donnelly, J. J., Polo, J. M., Barnett, S., Singh, M., Ulmer, J., and Dubensky, T. W.  
TITLE Microparticles for delivery of the heterologous nucleic acids  
JOURNAL Patent: WO 0226209-A 19 04-APR-2002;  
CHIRON CORPORATION (US)  
FEATURES  
source  
1. .22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Artificial sequence is synthesized"

BASE COUNT 6 a 3 c 7 g 6 t

ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGCAGATGA 20  
|||||  
8 GAACGTTGCAGATGA 22

RESULT 36  
AX592312 22 bp DNA linear PAT 27-JAN-2003  
LOCUS Sequence 2 from Patent WO02052002.  
ACCESSION AX592312  
VERSION AX592312.1 GI:27950414  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Fearon, K. L. and Dina, D.  
TITLE Immunomodulatory polynucleotides and methods of using the same  
JOURNAL Patent: WO 02052002-A 2 04-JUL-2002;  
DynaVax Technologies Corporation (US)  
FEATURES  
source  
1. .22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"

BASE COUNT 6 a 3 c 7 g 6 t

ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
 |||||  
 DB 8 GAACGTCGAGATGA 22

RESULT 37  
 AX592322 22 bp DNA linear PAT 27-JAN-2003  
 LOCUS Sequence 12 from Patent WO02052002.  
 AX592322  
 ACCESSION AX592322  
 VERSION AX592322.1 GI:27950424  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 FEATURES  
 1  
 REFERENCE  
 AUTHORS Fearon,K.L. and Dina,D.  
 TITLE Immunomodulatory polynucleotides and methods of using the same  
 JOURNAL Patent: WO 02052002-A 12 04-JUL-2002;  
 Dynavax Technologies Corporation (US)  
 FEATURES  
 1..22  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"  
 /note="Polynucleotide containing CG"

BASE COUNT 5 a 4 c 7 g 6 t  
 ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
 |||||  
 DB 8 GAACGTCGAGATGA 22

RESULT 38  
 AX592332 22 bp DNA linear PAT 27-JAN-2003  
 LOCUS Sequence 22 from Patent WO02052002.  
 AX592332  
 ACCESSION AX592332  
 VERSION AX592332.1 GI:27950434  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 FEATURES  
 1  
 REFERENCE  
 AUTHORS Fearon,K.L. and Dina,D.  
 TITLE Immunomodulatory polynucleotides and methods of using the same  
 JOURNAL Patent: WO 02052002-A 22 04-JUL-2002;  
 Dynavax Technologies Corporation (US)  
 FEATURES  
 1..22  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"  
 /note="Polynucleotide containing CG"

BASE COUNT 4 a 6 c 6 g 6 t  
 ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCGTGAACGTTTGA 15  
 |||||  
 DB 1 TCGTGAACGTTTGA 15

RESULT 39  
 AX592350 22 bp DNA linear PAT 27-JAN-2003  
 LOCUS Sequence 40 from Patent WO02052002.  
 AX592350  
 ACCESSION AX592350  
 VERSION AX592350.1 GI:27950452  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 FEATURES  
 1  
 REFERENCE  
 AUTHORS Fearon,K.L. and Dina,D.  
 TITLE Immunomodulatory polynucleotides and methods of using the same  
 JOURNAL Patent: WO 02052002-A 40 04-JUL-2002;  
 Dynavax Technologies Corporation (US)  
 FEATURES  
 1..22  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"  
 /note="Polynucleotide containing CG"

BASE COUNT 6 a 3 c 7 g 6 t  
 ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
 |||||  
 DB 8 GAACGTCGAGATGA 22

RESULT 40  
 AX592355 22 bp DNA linear PAT 27-JAN-2003  
 LOCUS Sequence 45 from Patent WO02052002.  
 AX592355  
 ACCESSION AX592355  
 VERSION AX592355.1 GI:27950457  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 FEATURES  
 1  
 REFERENCE  
 AUTHORS Fearon,K.L. and Dina,D.  
 TITLE Immunomodulatory polynucleotides and methods of using the same  
 JOURNAL Patent: WO 02052002-A 45 04-JUL-2002;  
 Dynavax Technologies Corporation (US)  
 FEATURES  
 1..22  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"  
 /note="Polynucleotide containing CG"

misc\_feature 2  
 /note="n = 5-bromocytosine"  
 misc\_feature 5  
 /note="n = 5-bromocytosine"  
 BASE COUNT 5 a 2 c 7 g 6 t  
 ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
 |||||  
 DB 8 GAACGTCGAGATGA 22

RESULT 41

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AX592356
LOCUS AX592356 22 bp DNA linear PAT 27-JAN-2003
DEFINITION Sequence 46 from Patent WO02052002.
ACCESSION AX592356
VERSION AX592356.1 GI:27950458
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Fearon, K.L. and Dina, D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 46 04-JUL-2002;
Dynavax Technologies Corporation (US)
FEATURES
source
1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"
misc_feature
5
/note="n = 5-bromocytosine"
BASE COUNT 5 a 3 c 7 g 6 t 1 others
ORIGIN
Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20
Db 8 GAACGTCGAGATGA 22

RESULT 42
LOCUS AX592369 22 bp DNA linear PAT 27-JAN-2003
DEFINITION Sequence 59 from Patent WO02052002.
ACCESSION AX592369
VERSION AX592369.1 GI:27950471
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Fearon, K.L. and Dina, D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 59 04-JUL-2002;
Dynavax Technologies Corporation (US)
FEATURES
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/organism="synthetic construct"
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/note="Polynucleotide containing CG"
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Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20
Db 8 GAACGTCGAGATGA 22

RESULT 43
LOCUS AX720306 22 bp DNA linear PAT 15-APR-2003
DEFINITION Sequence 1 from Patent WO03000032.
ACCESSION AX720306
VERSION AX720306.1 GI:29892140

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KEYWORDS
SOURCE
ORGANISM
REFERENCE
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AUTHORS Barenholz, Y., Kedari, E., Louria-Hayon, Y., Joseph, A., Raz, E. and
Takabayashi, K.
TITLE Method for preparation of vesicles loaded with immunostimulatory
oligodeoxynucleotides
JOURNAL Patent: WO 03000232-A 1 03-JAN-2003;
Viesum Research Development Company of the Hebrew Univ of Jerusalem
(IL); The Regents of the University of California (US)
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Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20
Db 8 GAACGTCGAGATGA 22

RESULT 44
LOCUS BD009235 22 bp DNA linear PAT 31-JAN-2002
DEFINITION Immunostimulatory polynucleotide/immunomodulatory molecule
conjugates.
ACCESSION BD009235
VERSION BD009235.1 GI:18637608
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Carson, D.A., Raz, E. and Roman, M.
TITLE Immunostimulatory polynucleotide/immunomodulatory molecule
JOURNAL Patent: JP 2001503254-A 34 13-MAR-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
COMMENT
OS Artificial Sequence
PN JP 2001503254-A/34
PD 13-MAR-2001
PF 09-OCT-1997 JP 1998518649
PR 11-OCT-1996 US 60/028118
PI DENNIS A CARSON, EYAL RAZ, MARK ROMAN
PC A61K39/00, A61K39/385, A61K39/39
CC
FH Key
FT source
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/mol_type="genomic DNA"
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BASE COUNT 6 a 3 c 7 g 6 t
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Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20
Db 8 GAACGTCGAGATGA 22

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RESULT 45  
BD182369 22 bp DNA linear PAT 15-MAY-2003  
LOCUS Anti-tumor antigens or their epitopes against HTLV-1 tumor.  
ACCESSION BD182369  
VERSION BD182369.1 GI:30793287  
KEYWORDS WO 02090981-A/1.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Hanabuchi,S., Ohashi,T. and Kannagi,M.  
TITLE Anti-tumor antigens or their epitopes against HTLV-1 tumor  
JOURNAL Patent: WO 02090981-A 1 14-NOV-2002;  
JAPAN SCIENCE AND TECHNOLOGY CORP,SHINO HANABUCHI,TAKASHI OHASHI,  
MARI KANNAGI  
COMMENT OS Artificial Sequence  
PN WO 02090981-A/1  
PD 14-NOV-2002  
PF 02-MAY-2002 WO 2002JP004406  
PR 08-MAY-2001 JP 01P 137526  
PI SHINO HANABUCHI,TAKASHI OHASHI,MARI KANNAGI  
PC GOIN3/50,GOIN3/15,AEIK39/00  
CC Description of Artificial Sequence:ISS-ODN  
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Qy 6 GAACGTTGAGATGA 20  
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Db 8 GAACGTTGAGATGA 22

RESULT 46  
AX083677/c 23 bp DNA linear PAT 28-FEB-2001  
LOCUS AX083677  
DEFINITION Sequence 3 from Patent WO0112223.  
ACCESSION AX083677  
VERSION AX083677.1 GI:13185409  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS van Nest,G.  
TITLE Methods of modulating an immune response using immunostimulatory s  
JOURNAL enquences and compositions for use therein  
Dynamax Technologies Corporation (US)  
FEATURES 1..23  
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RESULT 47  
AX148638 23 bp DNA linear PAT 08-JUN-2001  
LOCUS AX148638/c  
DEFINITION Sequence 3 from Patent WO0135991.  
ACCESSION AX148638  
VERSION AX148638.1 GI:14347256  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS Tuck,S. and van Nest,G.  
TITLE Immunomodulatory compositions containing an immunostimulatory  
JOURNAL sequence linked to antigen and methods of use thereof  
Dynamax Technologies Corporation (US)  
FEATURES 1..23  
source /organism="synthetic construct"  
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/note="synthetic construct"  
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RESULT 48  
AX250703/c 23 bp DNA linear PAT 05-OCT-2001  
LOCUS AX250703  
DEFINITION Sequence 3 from Patent WO0168078.  
ACCESSION AX250703  
VERSION AX250703.1 GI:15984441  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS van Nest,G.  
TITLE Methods of suppressing hepatitis virus infection using  
JOURNAL immunomodulatory polynucleotide sequences  
Dynamax Technologies Corporation (US)  
FEATURES 1..23  
source /organism="synthetic construct"  
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Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTTGAGATGA 20  
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Db 15 GAACGTTGAGATGA 1

RESULT 49



TITLE Methode of preventing and treating respiratory viral infection usi  
ng immunomodulatory polynucleotide sequences  
JOURNML Patent: WO 0168116-A 3 20-SEP-2001;  
DynaVax Technologies Corporation (US)  
FEATURES Location/Qualifiers  
source 1. 23  
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BASE COUNT 6 a 8 c 3 g 6 t  
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Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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15 GAACCTTCGAGATGA 1

RESULT 54  
AX253125/c 23 bp DNA linear PAT 05-OCT-2001  
LOCUS Sequence 3 from Patent WO0168077.  
DEFINITION AX253125  
ACCESSION AX253125  
VERSION AX253125.1 GI:15986293  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNML  
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BASE COUNT 6 a 8 c 3 g 6 t  
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15 GAACCTTCGAGATGA 1

RESULT 55  
AE007311 11033 bp DNA linear BCT 15-AUG-2001  
LOCUS Sinorhizobium meliloti plasmid pSymba section 117 of 121 of the  
DEFINITION complete plasmid sequence.  
ACCESSION AE007311 AE006469  
VERSION AE007311.1 GI:14524427  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
1 (Baees 1 to 11033)  
Barnett,M.J., Fisher,R.F., Jones,T., Komp,C., Abola,A.P.,  
Barloy-Hubler,F., Bowser,L., Capela,D., Galibert,F., Gouzy,J.,  
Gurjal,M., Hong,A., Huitzer,L., Hyman,R.W., Kahn,D., Kahn,M.L.,  
Kaiman,S., Keating,D.H., Palm,C., Peck,M.C., Surzycki,R.,  
Kalman,S., Keating,D.H., Palm,C., Peck,M.C., Surzycki,R.,

TITLE  
JOURNML  
MEDLINE  
PUBMED  
AUTHORS  
REFERENCE  
1 (bases 1 to 11033)  
Barnett,M.J., Fisher,R.F., Jones,T., Komp,C., Abola,A.P.,  
Barloy-Hubler,F., Bowser,L., Capela,D., Galibert,F., Gouzy,J.,  
Gurjal,M., Hong,A., Huitzer,L., Hyman,R.W., Kahn,D., Kahn,M.L.,  
Kaiman,S., Keating,D.H., Palm,C., Peck,M.C., Surzycki,R.,  
Wells,D.H., Yeh,K.-C., Davis,R.W., Federspiel,N.A. and Long,S.R.  
Direct Submission  
Submitted (29-MAR-2001) Biological Sciences, Stanford University,  
371 Serra Mall, Stanford, CA 94305, USA  
Location/Qualifiers  
1. 11033  
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71.4%; Score 15; DB 1; Length 11033;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match
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Db 3991 TCGTGAACGTTGCA 4005

RESULT 56
AF110737 11853 bp DNA linear BCT 03-APR-2001
LOCUS
DEFINITION Sinorhizobium meliloti strain 2011 rhizobactin regulon, complete
sequence.
ACCESSION AF110737
VERSION AF110737.1 GI:4151930
KEYWORDS Sinorhizobium meliloti
ORGANISM Sinorhizobium meliloti (Rhizobium meliloti)
REFERENCE 1
AUTHORS Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
1 (bases 1 to 11853)
Lynch,D., O'Brien,J., Welch,T., Clarke,P., Cui,Y.P.O., Crosa,J.H.
and O'Connell,M.
Genetic organization of the region encoding regulation,
biosynthesis, and transport of rhizobactin 1021, a siderophore
produced by Sinorhizobium meliloti
J. Bacteriol. 183 (8), 2576-2585 (2001)
JOURNAL MEDLINE
21172875
11274118
REFERENCE 2 (bases 1 to 11853)
Lynch,D., O'Connell,M. and O'Brien,J.
Cloning and sequence analysis of the Sinorhizobium meliloti 2011

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rhizobactin regulon  
unpublished  
3 (bases 1 to 11853)  
Lynch,D., O Connell,M. and O'Brien,J.  
Direct Submission  
Submitted (03-DEC-1998) School of Biotechnology, Dublin City  
University, Glasnevin, Dublin, Leinster Dublin 9, Ireland  
Location/Qualifiers  
1. .11853  
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GNFTSGGTOSMTALTYLAARCGPDKARAGVLTLSAHAFSIRKSAATLIGPAADAVIA  
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EASRRYSPEPAAAGPPLRMPAVSEDLRHTGSGSPSABEMLKRAMSDIDALAKPLP  
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MLKSLDVGITNSVRVNLARELDGDMYRFRRLHWODEFSRYPGILPLDPBFWGV  
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PLDIVADWFERPLTIFVRPIFGLYLHGHIMEAHQONIWEIIEHGPDIGLFYDNOG  
PFHERRAHGALVEALPGFSESVFGESEVPEDRLLVYAFINSYLGAMVAGLREGVLS  
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RIGIGYSDVLAFTENRTFTEVLMVGSKEKASFIABETLTNBSLVREAVGVSRESF  
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NLNAGSPSITDVAEAEHRTTPRAIOKFPSEREGTFERYVLGRSLSLALLEGATS
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ITKGRDAEPGLHAETVGTGMSGSGFASQDPBNAGATVYNSENNDAISLQNGRTG
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71.4%; Score 15; DB 1; Length 11853;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTCGACGTTGCA 15
Db 2511 TCGTCGACGTTGCA 2525

RESULT 57
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LOCUS Ancylostoma caninum metalloendopeptidase-1 (MEP-1) gene, partial
DEFINITION Ancylostoma caninum metalloendopeptidase-1 (MEP-1) gene, partial
ACCESSION AF381613
VERSION AF381613.1 GI:14549936
KEYWORDS Ancylostoma caninum (dog hookworm)
SOURCE Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
ORGANISM Ancylostoma caninum
REFERENCE 1 (bases 1 to 18662)
AUTHORS Jones,B.F. and Hotez,P.J.
TITLE Molecular cloning and characterization of Ac-mep-1, a
JOURNAL developmentally regulated gut luminal metalloendopeptidase from
Mol. Biochem. Parasitol. 119 (1), 107-116 (2002)
MEDLINE 216620013
PUBMED 11755191
REFERENCE 2 (bases 1 to 18662)
AUTHORS Jones,B.F. and Hotez,P.J.
TITLE Direct Submision
JOURNAL Submitted (17-MAY-2001) Department of Epidemiology and Public
Health, Yale University School of Medicine, 60 College St., New
Haven, CT 06510, USA
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SFOYLRHNNATDIGNRIGTYKDAODVNAEIVALEBVNVSDTKMSETERLVATLIF
TCVHTTRARKRDKNSKNVLIEMRDLFGIGIPRLNLTLLKNDIDFPDIMGKEQNHAGTL
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LDPSVPYIDMSRSARADVKLEQVIAASAPESLIRVYAOQHNRITDQLKRAIPAIK
WDSYFKALLSSVOQVDNKKONIILTOPSEFQMLNALRNGADDKTIANVLIHLIQE
ADPFGKALKTWQVAVPYALIRKGVTRGQOOLTRSHDPTVEDANVIOCLNSMTVM
PFGGVYVVKRRKRDVDVKDIEHOTELVFNPF"
BASE COUNT 5525 a 3765 c 3816 g 5389 t 167 others
ORIGIN

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
Db 10678 GAACGTTGAGATGA 10692

RESULT 58
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LOCUS Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***
DEFINITION AC013960
ACCESSION AC013960.1 GI:6437375
KEYWORDS HTG; HTGS_PHASE2
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 83321)
AUTHORS Adams,M. and Venter,J.C.
TITLE Direct Submision
JOURNAL Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT This sequence was identified as CDM:10210347 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a "working draft" sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
source
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 59  
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 DEFINITION Cyanidium caldarium strain Rkl chloroplast, complete genome.  
 ACCESSION AF022186 236235 270297  
 VERSION AF022186.2 GI:6466296  
 KEYWORDS  
 SOURCE chloroplast Cyanidium caldarium  
 ORGANISM Cyanidium caldarium  
 Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales;  
 Porphyridiaceae; Cyanidium.  
 1 (bases 130696 to 132364)  
 Vogel,H., Fischer,S. and Valentin,K.  
 A model for the evolution of the plastid sec apparatus inferred  
 from secY gene phylogeny  
 Plant Mol. Biol. 32 (4), 685-692 (1996)  
 97134960  
 MEDLINE 8980520  
 PUBMED  
 REFERENCE 2 (bases 1 to 164921)  
 Gloeckner,G., Rosenthal,A. and Valentin,K.  
 The structure and gene repertoire of an ancient red algal plastid  
 genome  
 J. Mol. Evol. 51 (4), 382-390 (2000)  
 20496959  
 MEDLINE  
 PUBMED  
 REFERENCE 3 (bases 46857 to 47851)  
 Valentin,K.  
 Direct Submision  
 Submitted (22-MAR-1996) Institute for Plant Physiology, Justus  
 Liebig University, Heinrich Buff Ring 58-62, Giessen 55392, Germany  
 4 (bases 28701 to 75580)  
 Gloeckner,G., Rosenthal,A. and Valentin,K.  
 Direct Submision  
 Submitted (02-SEP-1997) Department of Genome Analysis, IMB Jena,  
 Beutenbergstr. 11, Jena 07745, Germany  
 5 (bases 1 to 164921)  
 Gloeckner,G., Rosenthal,A. and Valentin,K.  
 Direct Submision  
 Submitted (18-NOV-1999) Genome Analysis, Institute for Molecular  
 Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany  
 6 (bases 130696 to 132364)  
 Vogel,H., Fischer,S. and Valentin,K.  
 Direct Submision  
 Submitted (18-NOV-1999) Institute for Plant Physiology, Justus  
 Liebig University, Heinrich Buff Ring 58-62, Giessen 55392, Germany  
 On or before Nov 23, 1999 this sequence version replaced gi:529651,  
 gi:1240002, gi:2465730.

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    Best Local Similarity 100.0%; Pred. No. 1.1e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 60
AC009346/c
LOCUS
DEFINITION
AC009346
VERSION
KEYWORDS
SOURCE
ORGANISM
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Mecoptera;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 168448)
REFERENCE
AUTHORS
Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Bazzon, J., Beeson, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Chape, M., Davenport, L.B., Dietz, S.M.,
Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Fartan, D.,
Ferreira, S., Frisoe, E., Galle, R.F., Garg, N.S., George, R.A.,
Gonzalez, M., Houch, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
Ibegwam, C., Jalali, M., Kruse, D., Li, P., Matel, B., Moshrefi, A.,
McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,
Pacled, J., Paragad, V., Park, S., Patel, S., Pfeiffer, B.,
Phouanavong, S., Piltman, G.S., Puri, V., Richards, S., Scheeler, F.,
Stapleton, M., Strong, R., Svitek, R., Tector, C., Williams, S.M.,
Zaveri, J.S., Smith, H.O., Rubin, G.M., and Venter, J.C.
Sequencing of Drosophila chromosome 3R, region 83A-83B
Unpublished
2 (bases 1 to 168448)
Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,
Butenoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
Doyle, C.M., Fartan, D.B., Galle, R., George, R.A., Harris, N.L.,
Hoskins, R.A., Houston, K.A., Hummasti, S.R., Katta, K., Kearney, L.,
Kim, B., Lee, B., Lewis, S., Li, P., Lomutan, M.A., Marda, P.,
Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacled, J., Pfeiffer, B.,
Pfeiffer, B., Poon, L., Sequiera, A., Sethi, H., Shit, E.,
Svitek, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
Rubin, G.M.
Direct Submission
Submitted (17-AUG-1999) Drosophila Genome Center, Lawrence Berkeley
Laboratory, MS 64-121, Berkeley, CA 94720, USA
On Feb 22, 2001 this sequence version replaced gi:7143384.
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
This sequence was assembled using end sequences from a whole genome
shotgun and from subclones of this BAC and its neighboring clones.
For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive web site (http://www.fruitfly.org/sequence/) or send email
to bdgp@fruitfly.berkeley.edu.
Location/Qualifiers
1..168448
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Drosophila melanogaster BAC library, partial EcoRI in
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BASE COUNT
46234 a 37731 c 38029 g 46454 t
ORIGIN
Query Match: 71.4%; Score 15; DB 3; Length 168448;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 59973 TCGTGAACGTTGGA 59959

RESULT 61  
SC0939126  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
JOURNAL  
COMMENT  
FEATURES

SC0939126 295150 bp DNA linear BCT 11-FEB-2003  
Streptomyces coelicolor A3(2) complete genome; segment 23/29  
AL0939126 AL0093517 AL023517 AL031514 AL034446 AL034492  
AL035212 AL035478 AL049727 AL132824 AL12997 AL589708 AL51522  
AL645882  
AL939126.1 GI:24413894

Streptomyces coelicolor A3(2)  
Streptomyces coelicolor A3(2)  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Streptomycinae; Streptomycetaceae; Streptomyces.

1  
Bentley, S.D., Chater, K.F., Cerdeno-Tarraga, A.M., Challis, G.L.,  
Thompson, N.R., James, K.D., Harris, D.E., Quail, M.A., Kiese, H.,  
Harper, D., Bateman, A., Brown, S., Chandra, G., Chen, C.W., Collins, M.,  
Cronin, A., Fraser, A., Goble, A., Hidalgo, J., Hornsby, T., Howarth, S.,  
Huang, C.H., Kiese, T., Larke, L., Murphy, L., Oliver, K., O'Neill, S.,  
Rabinowitsch, E., Rajandream, M.A., Rutherford, K., Rutter, S.,  
Seeger, K., Saunders, D., Sharp, S., Squares, R., Squares, S.,  
Taylor, K., Warren, T., Wietzorrek, A., Woodward, V., Barrell, B.G.,  
Parkhill, J., and Hopwood, D.A.  
Complete genome sequence of the model actinomycete Streptomyces  
coelicolor A3(2)  
Nature 417 (6885), 141-147 (2002)  
21996410  
12000953  
2 (bases 1 to 295150)  
Bentley, S.D.  
Direct Submision  
Submitted (09-MAY-2002) Submitted on behalf of the Streptomyces  
sequencing team, Sanger Institute, Wellcome Trust Genome Campus,  
Hinxton, Cambridge CB10 1SA E-mail: sdb@sanger.ac.uk  
On or before Oct 26, 2002 this sequence version replaced  
gi:20520744, gi:20520662, gi:20520663, gi:20520667, gi:20520669,  
gi:20520764, gi:20520816, gi:20520670, gi:20520820, gi:20520846,  
gi:20520823, gi:20520863, gi:20520869.  
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/strain="A3(2)"  
/db\_xref="taxon:100226"  
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/gene="SCO6005"  
/note="synonym: SC7B7.02"  
524..1933  
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/note="SC7B7.02, possible lipoprotein, len: 469; has  
similarity to signal sequence of Mycobacterium lepre  
hypothetical protein TR:E334742 (EMBL:298604) MLCB2052.27  
(445 aa), fasta scores; opt: 75 z-score: 199.2 E():  
0.00062, 23.3% identity in 335 aa overlap. Contains  
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fasta scores; opt: 393 z-score: 636.8 E(): 2.6e-28, 32.5%  
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GVSEELVPAKIDGAGRRTTISTIPAIRDSYVFAAYIGIALDALDFVVOANVPG  
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putative transport system permease protein from  
Clostridium perfringens (275 aa), fasta scores; opt: 590  
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3935..3984  
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Query Match 71.4%; Score 15; DB 1; Length 295150;  
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 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTCGACGTTGCA 15  
 Db 17025 TCGTCGACGTTGCA 17039

RESULT 62

AE003602/c  
 LOCUS 296091 bp DNA linear INV 14-FEB-2003  
 DEFINITION Drosophila melanogaster chromosome 3R, section 6 of 118 of the complete sequence.  
 ACCESSION AE003602 AE014297  
 VERSION AE003602.3 GI:23170357  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Drosophila melanogaster (fruit fly)  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 296091)  
 Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galle,R.F., George,R.A., Lewis,S.E., Richards,S., Ashburner,M., Henderson,S.N., Sutton,G.G., Wortman,J.R., Yeandle,M.D., Zhang,Q., Chen,L.X., Brandon,R.C., Rogers,Y.H., Blazer,V.G., Champs,M., Pfeiffer,B.D., Wan,K.H., Doyle,C., Baxter,E.G., Helt,G., Nelson,C.R., Gabor,G.L., Abell,J.F., Agbayani,A., Ah,R.J., Andrews-Fiankoch,C., Balwin,D., Ballew,R.M., Baau,A., Baxendale,J., Bayraktaroglu,L., Beasley,E.M., Beeson,K.Y., Benos,P.V., Berman,B.P., Bhandari,D., Bolshakov,S., Borkova,D., Botchan,M.R., Bouck,J., Brokstein,P., Brothier,P., Butte,K.C., Buam,D.A., Butler,H., Cadieu,E., Center,A., Chandra,I., Cherry,J.M., Cawley,S., Dahlke,C., Davenport,L.B., Davies,P., de Pablos,B., Delcher,A., Deng,Z., May,A.D., Dew,I., Dietz,S.M., Dodson,K., Doup,T.E., Downe,M., Dugan-Rocha,S., Dunkov,B.C., Dunn,P., Durbin,K.U., Evangelista,C.C., Ferrara,C., Ferriera,S., Fleischmann,W., Foster,C., Gabriellian,A.E., Garz,N.S., Gelbart,W.M., Glasser,K., Glodek,A., Gong,F., Gorrell,J.H., Gu,Z., Guan,P., Harris,M., Hattier,N.L., Harvey,D., Helman,T.J., Hernandez,J.R., Houch,J., Hoeltz,D., Houston,K.A., Howland,T.J., Wei,M.H., Ibegwam,C., Jalali,M., Kalush,F., Karpen,G.H., Ke,Z., Kemison,J.A., Ketchum,K.A., Kimmel,B.E., Kodira,C.D., Kraft,C., Kravitz,S., Kulp,D., Lai,Z., Lasko,P., Lei,Y., Levitsky,A.A., Li,J., Li,Z., Liang,Y., Lin,X., Liu,X., Matei,B., McIntosh,T.C., McLeod,M.P., McPherson,D., Mestrovic,G., Milshina,N.V., Mobarry,C., Morris,J., Moshrefi,A., Mount,S.M., Moy,M., Murphy,B., Murphy,L., Muzny,D.M., Nelson,D.L., Nelson,D.R., Nelson,K.A., Nixon,K., Nuskern,D.R., Paclelo,J.M., Palazolo,M., Pittman,G.S., Pan,S., Pollard,J., Puri,V., Reese,M.G., Reinert,K., Remington,K., Sanders,R.D., Scheeler,F., Shen,H., Shue,B.C., Sider-Kiamos,I., Simpson,M., Skupski,M.P., Smith,T., Spter,E., Spradling,A.C., Stempleton,M., Strong,R., Sun,E., Svirskas,R., Tector,C., Turner,R., Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wasserman,D.A., Weinstock,G.M., Weisenbach,J., Williams,S.M., Woodaet, Morley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yen,R.F., Zaveri,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H., Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O., Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.  
 The genome sequence of Drosophila melanogaster  
 Science 287 (5461), 2185-2195 (2000)

TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCES  
 AUTHORS

TITLE  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 2 (bases 1 to 296091)  
 Celniker,S.E., Adams,M.D., Kronmiller,B., Wan,K.H., Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C., Rogers,Y., Barzon,J.J., Ad,H., Baldwin,D., Barzon,K.Y., Bissam,D.A., Carlson,J.W., Center,A., Champs,M., Davenport,L.B., Dietz,S.M., Dodson,K., Dorset,V., Doup,L.E., Doyle,C., Dresnek,D., Fartan,D., Ferriera,S., Frise,E., Galle,R.F., Garz,N.S., George,R.A., Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J., Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A., McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J., Paclelo,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B., Phouanavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F., Stempleton,M., Strong,R., Svirskas,R., Tector,C., Tyler,D., Williams,S.M., Zaveri,J.S., Smith,H.O., Venter,J.C. and Rubin,G.M.  
 Sequencing of Drosophila melanogaster genome  
 Unpublished  
 3 (bases 1 to 296091)  
 Misra,S., Crosby,M.A., Matthews,B.B., Bayraktaroglu,L., Campbell,K., Hradecky,P., Huang,Y., Kaminker,J.S., Prochownik,S.E.,

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CDS		/complement (join(25096..25119,25188..25415,25541..25762) /locus_tag="CG2099" /note="CG2099 gene product" /codon_start=1 /product="CG2099-PA" /protein_id="AAFS2027_1" /db_xref="GI:7296748" /db_xref="FLYBASE:FBNM0037328"
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Db	190044 TCGTCGAAGCTTCCA 190030	
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Locus	AP005958	302650 bp DNA linear BCT 28-MAR-2003
DEFINITION	Bradyrhizobium japonicum USDA 110 DNA, complete genome, section	
	24/31.	
ACCSSION	AP005958 BA000040	
VERSION	AP005958.1 GI:727354550	
KEYWORDS		



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CTVPSRSLREAAAGFONCLMDPNTVEFGSNVEMADGVFTPADNGTFING  
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RHKPTKCFGVFAQTKTRHHPMDVPPRTFRIPHARMVVEEDLSDGYSVLTSAB  
AGVDCFVQOQNSLFVHFOGHPYEYTGSLGEGRDMGRFLGENEVCPTIPRGTLNK  
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Query Match 71.4%; Score 15; DB 1; Length 302650;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
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Qy 2 CGTCGACGCTTCG 16  
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Db 132468 CGTCGACGCTTCG 132454

RESULT 64  
AX592408 14 bp DNA linear PAT 27-JAN-2003  
DEFINITION Sequence 98 from Patent WO02052002.  
ACCESSION AX592408  
VERSION AX592408.1 GI:27950510  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS Fearon,K.L. and Dina,D.  
TITLE Immunomodulatory polynucleotides and methods of using the same  
JOURNAL Patent: WO 02052002-A 98 04-JUL-2002;  
Dynavax Technologies Corporation (US)

FEATURES Location/Qualifiers  
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BASE COUNT 2 a 4 c 4 g 4 t

ORIGIN

Query Match 66.7%; Score 14; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TCGTCGACGCTTCG 14

RESULT 65  
AX592321 16 bp DNA linear PAT 27-JAN-2003  
DEFINITION Sequence 11 from Patent WO02052002.  
ACCESSION AX592321  
VERSION AX592321.1 GI:27950423  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS Fearon,K.L. and Dina,D.  
TITLE Immunomodulatory polynucleotides and methods of using the same  
JOURNAL Patent: WO 02052002-A 11 04-JUL-2002;  
Dynavax Technologies Corporation (US)  
Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"

BASE COUNT 2 a 4 c 4 g 6 t

ORIGIN

Query Match 66.7%; Score 14; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGACGCTTCG 14  
|||||  
Db 1 TCGTCGACGCTTCG 14

RESULT 66  
AX592339 18 bp DNA linear PAT 27-JAN-2003  
DEFINITION Sequence 29 from Patent WO02052002.  
ACCESSION AX592339  
VERSION AX592339.1 GI:27950441  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.  
REFERENCE 1  
AUTHORS Fearon,K.L. and Dina,D.  
TITLE Immunomodulatory polynucleotides and methods of using the same  
JOURNAL Patent: WO 02052002-A 29 04-JUL-2002;  
Dynavax Technologies Corporation (US)  
Location/Qualifiers  
source 1..18  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"

misc\_feature 4

BASE COUNT 4 a /note="n = 5-bromocytosine"  
ORIGIN 3 c 5 g 1 others  
5 t

Query Match 66.7%; Score 14; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATG 19  
|||||  
Db 5 GAACGTCGAGATG 18

RESULT 67  
AX592354 18 bp DNA linear PAT 27-JAN-2003  
LOCUS AX592354  
DEFINITION Sequence 44 from Patent WO02052002.  
ACCESSION AX592354  
VERSION AX592354.1 GI:27950456  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
artificial sequences.  
REFERENCE  
AUTHORS Fearon,K.L. and Dina,D.  
TITLE Immunomodulatory polynucleotides and methods of using the same  
JOURNAL Patent: WO 02052002-A 44 04-JUL-2002;  
DynaVax Technologies Corporation (US)  
location/Qualifiers

FEATURES  
source 1..18  
1. 18  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"

BASE COUNT 4 a 3 c 6 g 5 t  
ORIGIN

Query Match 66.7%; Score 14; DB 6; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATG 19  
|||||  
Db 5 GAACGTCGAGATG 18

RESULT 68  
AX592333 19 bp DNA linear PAT 27-JAN-2003  
LOCUS AX592333  
DEFINITION Sequence 23 from Patent WO02052002.  
ACCESSION AX592333  
VERSION AX592333.1 GI:27950435  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
artificial sequences.  
REFERENCE  
AUTHORS Fearon,K.L. and Dina,D.  
TITLE Immunomodulatory polynucleotides and methods of using the same  
JOURNAL Patent: WO 02052002-A 23 04-JUL-2002;  
DynaVax Technologies Corporation (US)  
location/Qualifiers

FEATURES  
source 1..19  
1. 19  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"

misc\_feature 2  
/note="n = 5-bromocytosine"

misc\_feature 5  
/note="n = 5-bromocytosine"

BASE COUNT 4 a 2 c 6 g 5 t 2 others  
ORIGIN

Query Match 66.7%; Score 14; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATG 19  
|||||  
Db 6 GAACGTCGAGATG 19

RESULT 69  
AX592334 19 bp DNA linear PAT 27-JAN-2003  
LOCUS AX592334  
DEFINITION Sequence 24 from Patent WO02052002.  
ACCESSION AX592334  
VERSION AX592334.1 GI:27950436  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
artificial sequences.  
REFERENCE  
AUTHORS Fearon,K.L. and Dina,D.  
TITLE Immunomodulatory polynucleotides and methods of using the same  
JOURNAL Patent: WO 02052002-A 24 04-JUL-2002;  
DynaVax Technologies Corporation (US)  
location/Qualifiers

FEATURES  
source 1..19  
1. 19  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"

misc\_feature 5  
/note="n = 5-bromocytosine"

BASE COUNT 4 a 3 c 6 g 5 t 1 others  
ORIGIN

Query Match 66.7%; Score 14; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATG 19  
|||||  
Db 6 GAACGTCGAGATG 19

RESULT 70  
AX592365 20 bp DNA linear PAT 27-JAN-2003  
LOCUS AX592365  
DEFINITION Sequence 55 from Patent WO02052002.  
ACCESSION AX592365  
VERSION AX592365.1 GI:27950467  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
artificial sequences.  
REFERENCE  
AUTHORS Fearon,K.L. and Dina,D.  
TITLE Immunomodulatory polynucleotides and methods of using the same  
JOURNAL Patent: WO 02052002-A 55 04-JUL-2002;  
DynaVax Technologies Corporation (US)  
location/Qualifiers

FEATURES  
source 1..20  
1. 20  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"

BASE COUNT 4 a 4 c 7 g 5 t  
ORIGIN

Query Match 66.7%; Score 14; DB 6; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATG 19  
|||||  
Db 7 GAACGTCGAGATG 20

RESULT 71  
AX174913 22 bp DNA linear PAT 03-JUL-2001  
LOCUS AX174913  
DEFINITION Sequence 1 from Patent WO0143778.  
ACCESSION AX174913  
VERSION AX174913.1 GI:14598409  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE  
1 Felgner, P.L. and Zephari, O.  
AUTHORS Use of cationic lipids for intracellular protein delivery  
TITLE Patent: WO 0143778-A 1 21-JUN-2001;  
JOURNAL Gene Therapy Systems, Inc. (US)  
FEATURES  
source location/Qualifiers  
1..22  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Synthetic peptide"  
modified\_base 1  
/note="nT-NH2"  
/mod\_base=OTHER  
modified\_base 22  
/note="n=A-Rhodamine"  
/mod\_base=OTHER

BASE COUNT 5 a 7 g 5 t 2 others  
ORIGIN

Query Match 66.7%; Score 14; DB 6; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATG 19  
|||||  
Db 8 GAACGTCGAGATG 21

RESULT 72  
AX252517 24 bp DNA linear PAT 05-OCT-2001  
LOCUS AX252517  
DEFINITION Sequence 9 from Patent WO0168103.  
ACCESSION AX252517  
VERSION AX252517.1 GI:15985788  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE  
1 van Nee, G.  
AUTHORS Methods of ameliorating symptoms of herpes infection using  
TITLE immunomodulatory polynucleotide sequences  
JOURNAL Patent: WO 0168103-A 9 20-SEP-2001;  
Dynamax Technologies Corporation (US)  
FEATURES  
source location/Qualifiers  
1..24  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"

BASE COUNT 4 a 6 c 6 g 8 t  
ORIGIN

Query Match 66.7%; Score 14; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTGAACGTTG 14  
|||||  
Db 1 TCGTGAACGTTG 14

RESULT 73  
AX253133 24 bp DNA linear PAT 05-OCT-2001  
LOCUS AX253133  
DEFINITION Sequence 11 from Patent WO0168077.  
ACCESSION AX253133  
VERSION AX253133.1 GI:15986301  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE  
1 van Nee, G.  
AUTHORS Methods of preventing and treating viral infections using  
TITLE immunomodulatory polynucleotide sequences  
JOURNAL Patent: WO 0168077-A 11 20-SEP-2001;  
Dynamax Technologies Corporation (US)  
FEATURES  
source location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"

BASE COUNT 4 a 6 c 6 g 8 t  
ORIGIN

Query Match 66.7%; Score 14; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTGAACGTTG 14  
|||||  
Db 1 TCGTGAACGTTG 14

RESULT 74  
AX592311 24 bp DNA linear PAT 27-JAN-2003  
LOCUS AX592311  
DEFINITION Sequence 1 from Patent WO02052002.  
ACCESSION AX592311  
VERSION AX592311.1 GI:27950413  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
artificial sequences.

REFERENCE  
1 Fearon, K.L. and Dina, D.  
AUTHORS Immunomodulatory polynucleotides and methods of using the same  
TITLE Patent: WO 02052002-A 1 04-JUL-2002;  
JOURNAL Dynamax Technologies Corporation (US)  
FEATURES  
source location/Qualifiers  
1..24  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Polynucleotide containing CG"

BASE COUNT 4 a 6 c 6 g 8 t  
ORIGIN

Query Match 66.7%; Score 14; DB 6; Length 24;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTGAACGTTG 14  
|||||  
Db 1 TCGTGAACGTTG 14

RESULT 75

CNS018Y7  
 LOCUS 600 bp mRNA linear JUN 02-SEP-1999  
 DEFINITION Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation.  
 ACCESSION AL110950  
 VERSION AL110950.1 GI:5825237  
 KEYWORDS cDNA library; nitrogen deprivation.  
 SOURCE Botryotinia fuckeliana  
 ORGANISM Botryotinia fuckeliana  
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Sclerotiniaceae; Botryotinia.  
 1 (bases 1 to 600)  
 Helotiales; Sclerotiniaceae; Botryotinia.  
 Bitron, F., Lewis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.  
 REFERENCE Direct Submission  
 Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France  
 2 (bases 1 to 600)  
 REFERENCE Genoscope.  
 Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
 - Web : www.genoscope.cns.fr)  
 COMMENT The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII vector.  
 FEATURES  
 source Location/Qualifiers  
 1..600  
 /organism="Botryotinia fuckeliana"  
 /mol\_type="mRNA"  
 /strain="T4"  
 /db\_xref="taxon:40559"  
 /note="Genoscope sequence ID : W17H121"  
 BASE COUNT 189 a 103 c 137 g 171 t  
 ORIGIN  
 Query Match 66.7%; Score 14; DB 8; Length 600;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 ACGTCGAGATGAT 21  
 |||||||||  
 Db 248 ACGTCGAGATGAT 261

Search completed: December 17, 2003, 09:38:42  
 Job time : 1236 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 17, 2003, 09:15:24 / Search time 1313 Seconds  
(without alignments)  
386.724 Million cell updates/sec

Title: US-10-033-243-132

Perfect score: 21

Sequence: 1 tcgtcgaacttcgagatgatc 21

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estinu:\*  
4: em\_estnu:\*  
5: em\_estcov:\*  
6: em\_estcpl:\*  
7: em\_estcro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estcom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrt1:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result	No.	Score	Query	Match	Length	ID	Description
C 1	15	71.4	194	13	BU095678	BU095678 tca-163 t	
C 2	15	71.4	337	12	BI511039	BI511039	
C 3	15	71.4	390	9	AI945022	AI945022 b08b02.y	
C 4	15	71.4	432	12	BI510669	BI510669	

C 5	15	71.4	609	28	A0623639	A0623639 HS_5377_A
C 6	15	71.4	728	28	BH816458	BH816458 AM_Ba002
C 7	15	71.4	842	29	BZ391656	BZ391656 EINCQ64TR
C 8	15	71.4	889	14	CD375545	CD375545 PTMM00709
C 9	15	71.4	913	13	BK455352	BK455352 BK455352
C 10	15	71.4	1220	29	CC235774	CC235774 CH261-139
C 11	14	66.7	108	11	CNS09N54	BK066668 Single re
C 12	14	66.7	168	14	R04873	R04873 PK33h10.r1
C 13	14	66.7	298	9	AA186214	AA186214 T3860 MVA
C 14	14	66.7	348	11	CNS09O90	BK070096 Single re
C 15	14	66.7	387	12	BI507844	BI507844 BBI70008B
C 16	14	66.7	424	12	BI505056	BI505056 BBI70012B
C 17	14	66.7	414	14	CB333691	CB333691 T9ESTzyf6
C 18	14	66.7	433	12	BM629296	BM629296 170006874
C 19	14	66.7	439	28	AQ252378	AQ252378 HS_2262_A
C 20	14	66.7	466	14	CA302582	CA302582 taat13b12.
C 21	14	66.7	469	11	CNS09GNZ	BK057675 Single re
C 22	14	66.7	484	9	AA097939	AA097939 mnt82901.r
C 23	14	66.7	486	12	BM636144	BM636144 170006875
C 24	14	66.7	492	12	BM652631	BM652631 170006873
C 25	14	66.7	493	12	BM644091	BM644091 170006874
C 26	14	66.7	499	12	BM597612	BM597612 170006874
C 27	14	66.7	504	12	BM611518	BM611518 170006871
C 28	14	66.7	512	12	BM866297	BM866297 mgc8005XB
C 29	14	66.7	513	14	CB358730	CB358730 ZF001-P00
C 30	14	66.7	521	28	BH899325	BH899325 Oc800392
C 31	14	66.7	527	12	BM618536	BM618536 170006874
C 32	14	66.7	528	12	BM618261	BM618261 170006874
C 33	14	66.7	528	12	BM632494	BM632494 170006875
C 34	14	66.7	528	29	TA99D10P	TA99D10P T. brucei
C 35	14	66.7	533	12	BM641866	BM641866 170006873
C 36	14	66.7	534	28	AQ407920	AQ407920 HS_5055_B
C 37	14	66.7	541	9	AL65492	AL65492 AL65492_
C 38	14	66.7	544	12	BI511012	BI511012 BBI60004A
C 39	14	66.7	546	12	BM649585	BM649585 170006873
C 40	14	66.7	549	12	BM650226	BM650226 170006873
C 41	14	66.7	550	12	BM626834	BM626834 170006874
C 42	14	66.7	554	12	BM633500	BM633500 170006875
C 43	14	66.7	556	28	BH899413	BH899413 Oc800480
C 44	14	66.7	558	28	AZ216899	AZ216899 Sheared D
C 45	14	66.7	561	12	BM632387	BM632387 170006875
C 46	14	66.7	562	12	BM600003	BM600003 170006870
C 47	14	66.7	569	12	BM621639	BM621639 170006874
C 48	14	66.7	571	12	BM619639	BM619639 170006874
C 49	14	66.7	572	12	BM645614	BM645614 170006873
C 50	14	66.7	578	9	AL667035	AL667035 f224912.y
C 51	14	66.7	578	12	BM650798	BM650798 170006873
C 52	14	66.7	582	12	BM279238	BM279238 NB_ad1_04
C 53	14	66.7	583	10	BF157792	BF157792 F14905.y
C 54	14	66.7	588	12	BM630963	BM630963 170006875
C 55	14	66.7	592	12	BM649878	BM649878 170006873
C 56	14	66.7	593	12	BM624679	BM624679 170006874
C 57	14	66.7	595	12	BM622534	BM622534 170006874
C 58	14	66.7	595	12	BM632552	BM632552 170006875
C 59	14	66.7	600	12	BM639133	BM639133 170006875
C 60	14	66.7	601	28	AQ837727	AQ837727 HS_5413_B
C 61	14	66.7	606	12	BM621612	BM621612 170006874
C 62	14	66.7	606	28	BH416973	BH416973 1007052A0
C 63	14	66.7	614	12	BM634523	BM634523 170006875
C 64	14	66.7	616	12	BM625508	BM625508 170006874
C 65	14	66.7	617	28	AQ880074	AQ880074 HS_4867_A
C 66	14	66.7	619	12	BM591817	BM591817 170006874
C 67	14	66.7	627	29	CC120030	CC120030 NDJ_76020
C 68	14	66.7	628	9	AA288450	AA288450 mntmAd19
C 69	14	66.7	628	12	BM641079	BM641079 170006873
C 70	14	66.7	629	12	BM622163	BM622163 170006874
C 71	14	66.7	629	12	BM655453	BM655453 170006873
C 72	14	66.7	631	12	BM652565	BM652565 170006874
C 73	14	66.7	631	12	BM654222	BM654222 170006873
C 74	14	66.7	633	12	BM597192	BM597192 170006874
C 75	14	66.7	636	12	BM636272	BM636272 170006879
C 76	14	66.7	637	12	BM639355	BM639355 170006875
C 77	14	66.7	640	9	AL697586	AL697586

C	78	14	66.7	640	12	BM628043	170006874
C 79	14	66.7	645	12	BM620206	170006874	
C 80	14	66.7	655	12	BM600219	170006870	
C 81	14	66.7	655	12	BM591083	170006873	
C 82	14	66.7	658	12	BM650161	170006873	
C 83	14	66.7	659	12	BM646108	170006873	
C 84	14	66.7	660	12	BM646396	170006873	
C 85	14	66.7	660	12	BM655738	170006873	
C 86	14	66.7	662	12	BM585671	170006873	
C 87	14	66.7	662	12	BM634377	170006875	
C 88	14	66.7	662	12	BM635562	170006875	
C 89	14	66.7	666	12	BM577468	170006871	
C 90	14	66.7	667	12	BM623340	170006874	
C 91	14	66.7	670	12	BM639444	170006875	
C 92	14	66.7	671	12	BM619604	170006874	
C 93	14	66.7	672	12	BM638432	170006875	
C 94	14	66.7	672	12	BM656524	170006873	
C 95	14	66.7	673	12	BM619765	170006874	
C 96	14	66.7	677	12	BM636942	170006875	
C 97	14	66.7	680	12	BM623418	170006874	
C 98	14	66.7	681	13	BM6468200	170006874	
C 99	14	66.7	683	12	BM624318	170006874	
C 100	14	66.7	684	12	BM622788	170006874	

## ALIGNMENTS

RESULT 1  
BU095678/c 194 bp mRNA linear EST 14-MAR-2003  
LOCUS tca-163 tca Trypanosoma carassii cDNA clone 01n14 5', mRNA  
DEFINITION BU095678  
ACCESSION BU095678.1 GI:25123402  
KEYWORDS EST.

SOURCE Trypanosoma carassii  
ORGANISM Trypanosoma carassii  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.

REFERENCE 1 (bases 1 to 194)  
Aguero, F., Campo, V., Cremona, L., Jager, A., Di Noia, J.M., Overath, P.,  
Sanchez, D.O. and Frasch, A.C.  
Gene discovery in the freshwater fish parasite Trypanosoma  
carassii: identification of trans-sialidase-like and mucin-like  
genes

JOURNAL Infect. Immun. 70 (12), 7140-7144 (2002)  
COMMENT Contact: Sanchez DO  
Genomics and Bioinformatics  
Instituto de Investigaciones Bioteologicas  
Av. Gral Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martin, Buenos  
Aires, Argentina  
Tel: (54-11) 4580/7255/7  
Fax: (54-11) 4752-9639  
Email: dsanchez@ib.unsam.edu.ar  
Sequences were basecalled with phred and vector was masked with  
crossmatch (see http://www.phrap.org). Sequences were then trimmed  
from both ends to remove low quality bases and masked vector.  
Plate: 01 row: n column: 14  
Seq primer: T7

## FEATURES

source  
1..194  
/organism="Trypanosoma carassii"  
/mol\_type="mRNA"  
/db\_xref="taxon:38249"  
/clone="01n14"  
/dev\_stage="blood trypanosigote"  
/lab\_host="Goldfish (Carassius auratus)"  
/note="Vector: pSport1. Blood trypanosigotes were  
obtained from goldfish and cultured as described (Overath  
et al. Parasitol Res (1998) 84:343) before obtaining total  
RNA using TRIzol. cDNA library construction was made from

polyA+ mRNA using a poly-dT oligonucleotide as primer. The  
cDNAs were cloned in a oriented manner using a commercial  
kit (Superscript Plasmid System for cDNA Synthesis and  
Plasmid Cloning, Life Technologies)."

BASE COUNT 60 a 35 c 40 g 59 t  
Query Match 71.4%; Score 15; DB 13; Length 194;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 149 TCGTCGAACGTTCCA 135

RESULT 2  
B1511039/c 337 bp mRNA linear EST 08-APR-2002  
LOCUS B1511039  
DEFINITION B160004A20G12.5 Bee Brain Normalized Library, B16 Apis mellifera  
cDNA clone B160004A20G12 5', mRNA sequence.  
ACCESSION B1511039  
VERSION B1511039.1 GI:15361413  
KEYWORDS EST.  
SOURCE Apis mellifera (honeybee)  
ORGANISM Apis mellifera  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;  
Apoidea; Apis.

REFERENCE 1 (bases 1 to 337)  
Whitfield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L.,  
Pardinas, J., Robertson, H.M., Soares, B. and Robinson, G.E.  
Annotated expressed sequence tags and cDNA microarrays for studies  
of brain and behavior in the honey bee  
Genome Res. 12 (4), 555-566 (2002)  
21929762

JOURNAL MEDLINE  
COMMENT Contact: Gene E. Robinson  
Department of Entomology  
University of Illinois  
505 S. Goodwin Ave., Urbana, IL 61801, USA  
Tel: 217 265 0309  
Fax: 217 244 3499  
Email: gene@life.uiuc.edu  
This research was funded by the University of Illinois Critical  
Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation  
Award in Functional Genomics to G.E. Robinson and an NSF  
Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.  
PCR Primers  
FORWARD: TAATACGACTCCTATAGG  
BACKWARD: ATTACCCCTCACTAAG  
Plate: B160004A20 row: G column: 12  
Seq primer: AGCGATACATTTACACGCA  
High quality sequence stop: 337.

## FEATURES

source  
1..337  
/organism="Apis mellifera"  
/mol\_type="mRNA"  
/strain="mixed strains of European bees, predominantly  
A.m. ligustica"  
/db\_xref="taxon:7460"  
/clone="B160004A20G12"  
/sex="female"  
/tissue\_type="brain"  
/dev\_stage="adult worker honey bee"  
/lab\_host="DHI0B"  
/clone\_lib="Bee Brain Normalized Library, B16"  
/note="Organ: brain; Vector: pTR3-Pac; Site 1: EcORI;  
Site 2: NotI; The B16 library was contributed by the  
Soares laboratory and it was constructed and normalized  
as described by Bonaldo, M.F., Lennon, G. and Soares,  
M.B. (1996), Genome Research 6(9): 791-806. RNA was  
prepared from dissected brains of adult worker bees of



BASE COUNT 123 a 59 c 64 g 91 t various ages and various behavioral groups. "

Query Match 71.4%; Score 15; DB 12; Length 337;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCGTGAACGTTTGA 15  
|||||  
Db 264 TCGTGAACGTTTGA 250

RESULT 3  
A1945022/c 390 bp mRNA linear EST 08-JAN-2001

LOCUS b808b02.y1 Drosophila melanogaster adult testis library Drosophila  
DEFINITION melanogaster cDNA clone b808b02 5', mRNA sequence.

ACCESSION A1945022  
VERSION A1945022.2 GI:9990370  
KEYWORDS EST.  
SOURCE Drosophila melanogaster (fruit fly)

ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 390)  
Andrews, J., Bouffard, G.G., Cheadle, C., Lu, J., Becker, K.G. and  
Oliver, B.

TITLE Gene discovery using computational and microarray analysis of  
transcription in the drosophila melanogaster testis  
JOURNAL Genome Res. 10 (12), 2030-2043 (2000)  
MEDLINE 2058492  
PUBMED 1116097

COMMENT On Aug 17, 1999 this sequence version replaced gi:5735420.

Contact: Brian Oliver  
Laboratory of Cellular and Developmental Biology  
NIDDK, National Institutes of Health  
6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda, MD 20892 USA  
Fax: (301) 496 5239

Email: oliver@helix.nih.gov,  
http://www.nidk.nih.gov/intram/people/boliver.htm  
Tissue isolation and library construction performed at the National  
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see  
http://www.nidk.nih.gov/intram/people/boliver.htm). DNA sequencing  
and analyses performed by National Institutes of Health Intramural  
Sequencing Center (NISC; see http://www.nisc.nih.gov).

Plate: 08 row: b column: 02  
Seq primer: M13RPI reverse primer (ABT).

FEATURES  
Location/Qualifiers

1..390  
/organism="Drosophila melanogaster"  
/mol\_type="mRNA"  
/strain="y[\*] w[67c1]/Y"  
/db\_xref="taxon:7227"  
/clone="b808b02"  
/sex="male"  
/dev\_stage="1-5 day adult"  
/lab\_host="SOLR (Stratagene)"  
/note="Torgan: testis, Vector: pBluescript SK (Stratagene);  
Site\_1: EcoR I; Site\_2: Xho I; Testes dissected from 1-5  
day adult y[\*] w[67c1]/Y males raised at 25°C. RNA  
isolated using Trizol (Life Technologies) and a single  
round of Poly(A)+ selection using Oligotex (Qiagen). cDNA  
library constructed using Stratagene ZAP-cDNA synthesis  
kit. Oligo dt-primed, size fractionated -1-6 kb and  
directionally cloned at EcoRI and XhoI in Uni-ZAP XR.  
Following a single round of amplification pBluescript SK  
phagemids were mass excised. A distribution channel for  
clones is being sought, but not currently available.  
Requests for clones cannot be honored."

BASE COUNT 121 a 77 c 109 g 83 t

ORIGIN

Query Match 71.4%; Score 15; DB 9; Length 390;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCGTGAACGTTTGA 15  
|||||  
Db 94 TCGTGAACGTTTGA 80

RESULT 4  
B1510669 432 bp. mRNA linear EST 08-APR-2002

LOCUS B1510669/c  
DEFINITION B160003A20G01.5 Bee Brain Normalized Library, B16 Apis mellifera  
cDNA clone B160003A20G01 5', mRNA sequence.

ACCESSION B1510669  
VERSION B1510669.1 GI:15361043  
KEYWORDS EST.  
SOURCE Apis mellifera (honeybee)

ORGANISM Apis mellifera  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;  
Apoidea; Apis.  
1 (bases 1 to 432)  
Whitfield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L.,  
Pardinas, J., Robertson, H.M., Soares, B. and Robinson, G.E.  
Annotated expressed sequence tags and cDNA microarrays for studies  
of brain and behavior in the honey bee  
Genome Res. 12 (4), 555-566 (2002)  
MEDLINE 21929762  
PUBMED 11932240

COMMENT Contact: Gene E. Robinson  
Department of Entomology  
University of Illinois  
505 S. Goodwin Ave., Urbana, IL 61801, USA  
Tel: 217 265 0309  
Fax: 217 244 3499  
Email: gene@life.uiuc.edu

This research was funded by the University of Illinois Critical  
Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation  
Award in Functional Genomics to G.E. Robinson and an NSF  
Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.

PCR Primers  
FORWARD: TAATGCGCTCACTATGCG  
BACKWARD: ATTACCTCCTACTAAG  
Plate: B160003A20 row: G column: 01  
Seq primer: AGCGATTAACAATTCACACAGA

High quality sequence stop: 432.

FEATURES  
Location/Qualifiers

1..432  
/organism="Apis mellifera"  
/mol\_type="mRNA"  
/strain="mixed strains of European bees, predominantly  
A.m. ligustica"  
/db\_xref="taxon:7460"  
/clone="B160003A20G01"  
/sex="female"  
/tissue\_type="brain"  
/dev\_stage="adult worker honey bee"  
/lab\_host="BD10B"

/note="Organ: brain; Vector: pT73-Pac; Site\_1: EcoRI;  
Site\_2: NotI; The B16 library was constructed and normalized  
as described by Bonaldo, M.F., Lennon, G. and Soares,  
M.B. (1996). Genome Research 6(9): 791-806. RNA was  
prepared from dissected brains of adult worker bees of  
various ages and various behavioral groups."

BASE COUNT 163 a 69 c 102 g 98 t

Query Match 71.4%; Score 15; DB 12; Length 432;

Best Local Similarity 100.0%; Pred. No. 80;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCGTCGAACGTTGCA 15  
|||||  
Db 58 TCGTCGAACGTTGCA 44

RESULT 5  
AO623639 609 bp DNA linear GSS 16-JUN-1999  
LOCUS  
DEFINITION HS\_5377\_A2\_F05 SPE6 RPCT-11 Human Male BAC Library Homo sapiens  
genomic clone Plate=953 Col=10 Row=K, genomic survey sequence.  
ACCESSION AO623639  
VERSION AO623639.1 GI:5086119  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 609)  
Mahairas,G., Wallace,J.C., Smith,K., Swartzell,S., Holman,T.,  
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
Hood,L.  
Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
JOURNAL MEDLINE 99380589  
PubMed 10449764  
COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones are derived from the human BAC library RPCT-11. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACpac Resources (http://bacpac.med.buffalo.edu/ordering\_bac.htm)  
or from Research Genetics (info@resgen.com). BAC end web server:  
http://www.htsc.washington.edu  
Plate: 953 row: K column: 10  
Seq primer: SP6  
Class: BAC ends  
High quality sequence stop: 609.  
Location/Qualifiers  
1..609  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="Plate=953 Col=10 Row=K"  
/sex="male"  
/clone\_lib="RPCT-11 Human Male BAC Library"  
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;  
Male blood DNA was isolated from one randomly chosen donor  
and partially digested with a combination of EcoRI and  
EcoRI Methylase. Size selected DNA was cloned into the  
pBACe3.6 vector at EcoRI sites"

BASE COUNT 185 a 124 c 162 g 125 t 13 others

ORIGIN  
Query Match 71.4%; Score 15; DB 28; Length 609;  
Best Local Similarity 100.0%; Pred. No. 84;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCGTCGAACGTTGCA 15  
|||||  
Db 335 TCGTCGAACGTTGCA 349

RESULT 6  
BH816458

LOCUS BH816458 728 bp DNA linear GSS 08-MAY-2002  
DEFINITION AM\_BA0021J24f Apis mellifera Apis mellifera genomic clone  
AM\_BA0021J24f, genomic survey sequence.  
ACCESSION BH816458  
VERSION BH816458.1 GI:20512115  
KEYWORDS GSS.  
SOURCE Apis mellifera (honeybee)  
ORGANISM Apis mellifera  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;  
Apidae; Apis.  
REFERENCE 1 (bases 1 to 728)  
Tomkins,J.P., Luo,M., Hunt,G., Main,D., Erisch,D., Page,P.E.,  
Guzman-Nova,E. and Wing,R.A.  
Development of Genomic Resources for honey bee (Apis mellifera L.):  
BAC Library Construction, Preliminary STC Analysis, and  
Identification of Clones Associated With Behavioral Traits  
Unpublished  
Contact: Tomkins JP  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson University, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: jtomkins@clemson.edu  
Total hg bases = 231  
Seq primer: TAATGACACTGACTATAGGG  
Class: BAC ends  
High quality sequence start: 52  
High quality sequence stop: 502.  
Location/Qualifiers  
1..728  
/organism="Apis mellifera"  
/mol\_type="genomic DNA"  
/strain="Africanized honey bee"  
/db\_xref="taxon:7460"  
/clone="AM\_BA0021J24f"  
/tissue\_type="larva"  
/lab\_host="E. coli"  
/clone\_lib="Apis mellifera"  
/note="Vector: pCUTBAC-1; Site 1: HindIII; Site 2: NotI;  
For more details on library preparation and sequence  
analysis see  
http://www.genome.clemson.edu/projects/stc/bee/AM\_Ba/ to  
order clones from this library see  
http://www.genome.clemson.edu/orders "

BASE COUNT 227 a 134 c 156 g 207 t 4 others

ORIGIN  
Query Match 71.4%; Score 15; DB 28; Length 728;  
Best Local Similarity 100.0%; Pred. No. 86;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACCTTGAGATGA 20  
|||||  
Db 118 GAACCTTGAGATGA 132

RESULT 7  
BZ391656/c 842 bp DNA linear GSS 30-APR-2003  
LOCUS  
DEFINITION EINC064TR EI 10 12 KB Entamoeba invadens genomic clone EINC064,  
genomic survey sequence.  
ACCESSION BZ391656  
VERSION BZ391656.1 GI:30238193  
KEYWORDS GSS.  
SOURCE Entamoeba invadens  
ORGANISM Entamoeba invadens  
Eukaryota; Entamoebidae; Entamoeba.  
REFERENCE 1 (bases 1 to 842)  
Loftus,B., Wang,Z., Roncaglia,P., Van Aken,S. and Fraser,C.  
Gene discovery in the Entamoeba invadens genome  
Unpublished

```
COMMENT
Other GSSs: EINC0647F
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
DNA was provided by Daniel Eichinger
Seq primer: TR
Class: sheared ends.

FEATURES
source
1..842
/organism="Entamoeba invadens"
/mol_type="genomic DNA"
/strain="IP-1"
/db_xref="taxon:33085"
/clone="EINC064"
/clone_1ib="EI.10.12 KB"
/note="Vector: pHOS2; Site 1: BstXI; Total genomic DNA was
isolated from early log phase trophozoites of E. invadens
IP-1 using a Qiagen plant DNA extraction kit. A shotgun
medium-size plasmid library (average insert size of 10 -
12 kb) was generated by random mechanical shearing of E.
invadens genomic DNA, repairing the ends of DNA fragments
with T4 Polymerase, adding BstXI adaptors and ligating
into the BstXI site of a pUC-derived vector pHOS2."

BASE COUNT
281 a 152 c 140 g 269 t

ORIGIN
Query Match 71.4%; Score 15; DB 29; Length 842;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AACGTTGAGATGAT 21
|||||
796 AACGTTGAGATGAT 782

Db

RESULT 8
CD375545 889 bp mRNA linear EST 31-MAY-2003
LOCUS CD375545
DEFINITION PTM00709 Phaeodactylum tricornutum Uni-Zap XR Phaeodactylum
tricornutum cDNA 5', mRNA sequence.
ACCESSION CD375545
VERSION CD375545.1 GI:31251159
KEYWORDS EST.
SOURCE Phaeodactylum tricornutum
ORGANISM Phaeodactylum tricornutum
Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
Bacillariophycidae; Naviculales; Phaeodactylaceae; Phaeodactylum.
1 (bases 1 to 889)
Scalà,S., Carels,N., Falciatore,A., Chiusano,M.L. and Bowler,C.
Genome properties of the diatom Phaeodactylum tricornutum
Plant Physiol. 129 (3), 993-1002 (2002)
2211123
1211455
12114555
Contact: Bowler C
Laboratory of Molecular Plant Biology
Stazione Zoologica 'Anton Dohrn'
Villa Comunale, I-80121, Napoli, Italy
Tel: 39 081 583 3268/3211
Fax: 39 081 764 1355
Email: christel@na.szn.it
Diatom EST Database(http://aves.thagen.sznbowlr.com)
Seq primer: T3 backward
POLYA=yes.

FEATURES
source
1..889
/location/Qualifiers
/organism="Phaeodactylum tricornutum"
/mol_type="mRNA"
/db_xref="taxon:2850"
/cell_line="CIMP632"

COMMENT
Other GSSs: EINC0647F
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
DNA was provided by Daniel Eichinger
Seq primer: TR
Class: sheared ends.

FEATURES
source
1..842
/organism="Entamoeba invadens"
/mol_type="genomic DNA"
/strain="IP-1"
/db_xref="taxon:33085"
/clone="EINC064"
/clone_1ib="EI.10.12 KB"
/note="Vector: pHOS2; Site 1: BstXI; Total genomic DNA was
isolated from early log phase trophozoites of E. invadens
IP-1 using a Qiagen plant DNA extraction kit. A shotgun
medium-size plasmid library (average insert size of 10 -
12 kb) was generated by random mechanical shearing of E.
invadens genomic DNA, repairing the ends of DNA fragments
with T4 Polymerase, adding BstXI adaptors and ligating
into the BstXI site of a pUC-derived vector pHOS2."

BASE COUNT
281 a 152 c 140 g 269 t

ORIGIN
Query Match 71.4%; Score 15; DB 29; Length 842;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AACGTTGAGATGAT 21
|||||
796 AACGTTGAGATGAT 782

Db

RESULT 9
BX455352 913 bp mRNA linear EST 22-MAY-2003
LOCUS BX455352
DEFINITION CSDDP022YA13 3-PRIME, mRNA sequence.
ACCESSION BX455352
VERSION BX455352.1 GI:31019187
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 913)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10667.f. For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSDBAK038CA04NM2&cluster=10667.f. Contact :
Feng liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSDBAK038CA04NM2.

FEATURES
source
1..913
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSDDP022YA13"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_1ib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dt) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoR sites of the pCMVSPORT 6
vector. Library was not normalized."

BASE COUNT
304 a 199 c 163 g 246 t

ORIGIN
Query Match 71.4%; Score 15; DB 13; Length 913;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTTGAGATGA 20
|||||
900 GAACGTTGAGATGA 886

Db

RESULT 10
CC235774 1220 bp DNA linear GSS 12-MAY-2003
LOCUS CC235774
DEFINITION CH261-139L19_RM1.2 CH261 Gallus gallus genomic clone CH261-139L19,
```

genomic survey sequence.  
ACCESSION CC35774  
VERSION CC235774.1 GI:30562437  
KEYWORDS GSS.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
REFERENCE 1 (bases 1 to 1220)  
Kremtchik, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,  
Warren, W., Graves, T., Mardis, E. and Wilson, R.  
Gallus gallus BAC End Reads  
JOURNAL Unpublished  
COMMENT Contact: Richard K. Wilson  
Genome Sequencing Center  
Washington University School of Medicine  
Email: submissions@watson.wustl.edu  
Insert Length: 18200 Std Error: 0.00  
Seq primer: RM1 TACGACTCAGCTATGCGAGA  
Class: BAC ends  
High quality sequence start: 473  
High quality sequence stop: 541.  
Location/Qualifiers  
1..1220  
/organism="Gallus gallus"  
/mol\_type="genomic DNA"  
/strain="Red Jungle Fowl"  
/db\_xref="taxon:9031"  
/clone="CH261-139A19"  
/sex="female"  
/cell\_line="UICD001, inbred 256"  
/clone\_1ib="CH261"  
/note="Vector: PTARBAC2.1; Site 1: EcorI; Site 2: EcorI;  
CH261 Female Chicken library - for library and clone  
ordering information: <http://www.chori.org/bacpac>"

BASE COUNT 320 a 330 c 171 g 399 t  
ORIGIN

Query Match 71.4%; Score 15; DB 29; Length 1220;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AACGTTCCGAGATGAT 21  
|||||  
461 AACGTTCCGAGATGAT 447

Db 461 AACGTTCCGAGATGAT 447

RESULT 11 108 bp mRNA linear HTC 08-JAN-2003  
CNS09N54  
LOCUS CNS09N54/C  
DEFINITION Single read from an extremity of a full-length cDNA clone made from  
Anopheles gambiae total adult females. 5-PRIME end of clone  
FK0AACA5A09 of strain 6-9 of Anopheles gambiae (African malaria  
mosquito).  
ACCESSION BX066068  
VERSION BX066068.1 GI:27639349  
KEYWORDS HTC.  
SOURCE Anopheles gambiae (African malaria mosquito)  
ORGANISM Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
Anopheles.  
REFERENCE 1 (bases 1 to 108)  
Genoscope.  
Direct Submission  
Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : [secref@genoscope.cns.fr](mailto:secref@genoscope.cns.fr))  
- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
Location/Qualifiers  
1..108  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"

FEATURES  
Source

/strain="6-9"  
/db\_xref="taxon:7165"  
/clone="FK0AACA5A09"  
/plasmid="pME18-FL"  
/note="end : 5-PRIME"

BASE COUNT 21 a 31 c 34 g 22 t  
ORIGIN

Query Match 66.7%; Score 14; DB 11; Length 108;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGAACGTTCCGAGAT 18  
|||||  
61 CGAACGTTCCGAGAT 48

Db 61 CGAACGTTCCGAGAT 48

RESULT 12 168 bp mRNA linear EST 31-MAR-1995  
R04873  
LOCUS R04873  
DEFINITION pk33h10.r1 Kuwabara Mixed stage C. briggsae Caenorhabditis briggsae  
cDNA, mRNA sequence.  
ACCESSION R04873  
VERSION R04873.1 GI:754609  
KEYWORDS EST.  
SOURCE Caenorhabditis briggsae  
ORGANISM Caenorhabditis briggsae  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea  
; Rhabditidae; Peloderinae; Caenorhabditis.  
REFERENCE 1 (bases 1 to 168)  
Hillier, L., Chippelli, B., Chissee, S., Clark, N., Couch, J., Dubuque  
T., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Kuwabara, P., Le  
, M., Mardis, E., Marra, M., Parsons, J., Rifkin, B., Rohlfing, T., Tan  
, F., Treviski, E., Waterston, R., Wohlmann, P. and Wilson, R.  
Washington University Caenorhabditis briggsae EST project  
JOURNAL Unpublished  
COMMENT Contact: Marra MA  
Washington University Genome Sequencing Center  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1455  
Fax: 314 286 1810  
Email: [mmarra@watson.wustl.edu](mailto:mmarra@watson.wustl.edu)  
PCR F: TGTAACAGCAGCGCAGTAGCAGTTCAGCTCG  
PCR B: CAGGAACAGCTATGACCTTAGCTATTCCTCAGGGA  
Source: Washington University Genome Sequencing Center  
PCR amplified DNA is available from Washington University Genome  
Sequencing Center. Aliquots of the library may be requested from P.  
Kuwabara ([pekemrc-lmb.cam.ac.uk](mailto:pekemrc-lmb.cam.ac.uk)).  
Seq primer: Commercially available M13 reverse dye primer.  
Location/Qualifiers  
1..168  
/organism="Caenorhabditis briggsae"  
/mol\_type="mRNA"  
/strain="G16 Gujarat"  
/db\_xref="taxon:6238"  
/clone\_1ib="Kuwabara Mixed stage C. briggsae"  
/note="Vector: lambda g10; Site 1: EcorI; Site 2: EcorI;  
Stage:mixed, Sex:hermaphrodite. Library construction:  
First strand oligo(dT) primed. Second strand was as per  
Gubler/Hoffman. Ligated to EcorI adaptors. Library is  
non-directional. Library is non-normalized. Library  
constructed by P.E. Kuwabara. Additional details on  
construction of the library are described in P.E.  
Kuwabara and S. Shah, NAR 22: 4414 - 4418 (1994). Adaptor  
sequence: GAATTC CGTTGCTGTC"

BASE COUNT 46 a 42 c 42 g 38 t  
ORIGIN

Query Match 66.7%; Score 14; DB 14; Length 168;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGACGCTCG 14  
 |||||  
 Db 148 TCGTCGACGCTCG 161

RESULT 13  
 AA186214 298 bp mRNA linear EST 10-JAN-1997  
 LOCUS AA186214/c  
 DEFINITION T3860 MVAT4 bloodstream form of serodeme WRATat.1 Trypanosoma  
 brucei rhodesiense cDNA 5', mRNA sequence.  
 ACCESSION AA186214  
 VERSION AA186214.1 GI:1772670  
 KEYWORDS EST.  
 SOURCE Trypanosoma brucei rhodesiense  
 ORGANISM Trypanosoma brucei rhodesiense  
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.

REFERENCE  
 AUTHORS Djikeng, A., Donelson, J.E. and Majiwa, P.A.O.  
 TITLE Generation of expressed sequence tags as physical landmarks in the  
 genome of Trypanosoma brucei  
 JOURNAL Unpublished  
 COMMENT Contact: Majiwa PAO  
 Molecular Biology Unit  
 International Livestock Research Institute  
 P.O. Box 30709, Nairobi, Kenya  
 Tel: 254-2 630743  
 Fax: 254-2 631499  
 Email: p.majiwa@cnet.com  
 Seq primer: T3 primer.  
 Location/Qualifiers

FEATURES  
 source  
 1..298  
 /organism="Trypanosoma brucei rhodesiense"  
 /mol\_type="mRNA"  
 /sub\_species="rhodesiense"  
 /db\_xref="taxon:31286"  
 /clone\_lib="MVAT4 bloodstream form of serodeme WRATat.1"  
 /note="Vector: lambda ZAP II (Stratagene); Site 1: EcoRI;  
 Site 2: XhoI; The mRNA was purified from a cloned  
 population of bloodstream trypanosomes reexpressing the  
 MVAT4 metacyclic variant surface glycoprotein (VSG). A  
 unidirectional oligo dT-primed EcoRI/XhoI cDNA library was  
 constructed in lambda ZAP II (Stratagene)."

BASE COUNT 93 a 63 c 86 g 56 t  
 ORIGIN

Query Match 66.7%; Score 14; DB 9; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACCTTCGAGATGAT 21  
 |||||  
 Db 263 ACCTTCGAGATGAT 250

RESULT 14  
 CDS0090/c 348 bp mRNA linear HTC 08-JAN-2003  
 LOCUS CDS0090/c  
 DEFINITION Single read from an extremity of a full-length cDNA clone made from  
 Anopheles gambiae total adult females. 5-PRIME end of clone  
 FK0AC7AB01 of strain 6-9 of Anopheles gambiae (African malaria  
 mosquito).  
 ACCESSION BX070056  
 VERSION BX070056.1 GI:27643377  
 KEYWORDS HTC.  
 SOURCE Anopheles gambiae (African malaria mosquito)  
 ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
 Anopheles.  
 REFERENCE 1 (bases 1 to 348)  
 AUTHORS Genoscope.  
 TITLE Direct Submission

JOURNAL  
 Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage :  
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
 - Web : www.genoscope.cns.fr

FEATURES  
 source  
 1..348  
 /organism="Anopheles gambiae"  
 /mol\_type="mRNA"  
 /strain="6-9"  
 /db\_xref="taxon:7165"  
 /clone="FK0AC7AB01"  
 /plasmid="pME18S-FL"  
 /note="end : 5-PRIME"

BASE COUNT 81 a 101 c 114 g 52 t  
 ORIGIN

Query Match 66.7%; Score 14; DB 11; Length 348;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGACGTCGAGAT 18  
 |||||  
 Db 263 CGACGTCGAGAT 250

RESULT 15  
 B1507844 387 bp mRNA linear EST 08-APR-2002  
 LOCUS B1507844  
 DEFINITION B170008B10E04.5 Bee Brain Normalized/Subtracted Library, B17 Apis  
 mellifera cDNA clone B170008B10E04 5', mRNA sequence.  
 ACCESSION B1507844  
 VERSION B1507844.1 GI:15358218  
 KEYWORDS EST.  
 SOURCE Apis mellifera (honeybee)  
 ORGANISM Apis mellifera  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Hymenoptera; Apoidea; Aculeata; Apoidea;  
 Apidae; Apis.

REFERENCE  
 AUTHORS Whitfield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L.,  
 Partins, J., Robertson, H.M., Soares, B. and Robinson, G.E.  
 TITLE Annotated expressed sequence tags and cDNA microarrays for studies  
 of brain and behavior in the honey bee  
 JOURNAL Genome Res. 12 (4), 555-566 (2002)  
 MEDLINE 21929762  
 PUBMED 11932240

COMMENT  
 Contact: Gene E. Robinson  
 Department of Entomology  
 University of Illinois  
 505 S. Goodwin Ave., Urbana, IL 61801, USA  
 Tel: 217 265 0309  
 Fax: 217 244 3493  
 Email: genrob@life.uiuc.edu  
 This research was funded by the University of Illinois Critical  
 Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation  
 Award in Functional Genomics to G.E. Robinson and an NSF  
 Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.  
 PCR PRIMERS  
 FORWARD: TAAATGACACTGACTATAGG  
 BACKWARD: ATTATCCCTCCTAAG  
 Plate: B170008B10 row: E column: 04  
 Seq primer: AGCGATACATTTACACAGGA  
 High quality sequence stop: 387.  
 Location/Qualifiers

FEATURES  
 source  
 1..387  
 /organism="Apis mellifera"  
 /mol\_type="mRNA"  
 /strain="mixed strains of European bees, predominantly  
 A.m. ligustica"  
 /db\_xref="taxon:7460"  
 /clone="B170008B10E04"  
 /sex="female"  
 /tissue\_type="brain"  
 /dev\_stage="adult worker honey bee"

/lab\_host="DH10B"  
/clone\_lib="Bee Brain Normalized/Subtracted Library, BB17"  
/note="Organ: Brain; Vector: pRT3-Pac; Site 1: EcotRI;  
Site 2: NotI; This BB17 CDNA library was generated by  
subtraction of the BB16 library with 4000 previously  
sequenced clones. The BB16 library was contributed by the  
Soares laboratory and it was constructed and normalized  
as described by Bonaldo, M.F., Lennon, G. and Soares,  
M.B. (1996), Genome Research 6(9): 791-806. RNA was  
prepared from dissected brains of adult worker bees of  
various ages and various behavioral groups."

BASE COUNT 125 a 71 c 95 g 96 t  
ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 387;  
Best Local Similarity 100.0%; Pred. No. 3e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 AGCTTCGAGATGAT 21  
|||||  
228 ACCTTCGAGATGAT 241

RESULT 16 414 bp mRNA linear EST 08-APR-2002  
BI505056 BB170012B20C02.5 Bee Brain Normalized/Subtracted Library, BB17 Apis  
LOCUS mellifera CDNA clone BB170012B20C02 5', mRNA sequence.  
DEFINITION  
ACCESSION BI505056  
VERSION BI505056.1 GI:15355430  
KEYWORDS EST.  
SOURCE Apis mellifera (honeybee)  
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;  
Apidae; Apis.  
1 (bases 1 to 414)  
Whitfield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L.,  
Pardinas, J.D., Robertson, H.M., Soares, B. and Robinson, G.E.  
Annotated expressed sequence tags and cDNA microarrays for studies  
of brain and behavior in the honey bee  
Genome Res. 12 (4), 555-566 (2002)

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

CONTACT: Gene E. Robinson  
Department of Entomology  
University of Illinois  
505 S. Goodwin Ave., Urbana, IL 61801, USA  
Tel: 217 265 0309  
Fax: 217 244 3499  
Email: generobi@life.uiuc.edu  
This research was funded by the University of Illinois Critical  
Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation  
Award in Functional Genomics to G.E. Robinson and an NSF  
Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.  
PCR Primers  
FORWARD: ATATACGACTCACTAAGG  
BACKWARD: TATACCTCTACTAAG  
Plate: BB170012B20 row: C column: 02  
Seq primer: AGCGGATACCAATTCACACAGA  
High quality sequence stop: 414.  
Location/Qualifiers  
1. 414  
/organism="Apis mellifera"  
/mol\_type="mRNA"  
/strain="mixed strains of European bees, predominantly  
A.m. ligustica"  
/db\_xref="taxon:7460"  
/clone="BB170012B20C02"  
/sex="female"  
/tissue\_type="brain"  
/dev\_stage="adult worker honey bee"  
/lab\_host="DH10B"

FEATURES  
source

/clone\_lib="Bee Brain Normalized/Subtracted Library, BB17"  
/note="Organ: Brain; Vector: pRT3-Pac; Site 1: EcotRI;  
Site 2: NotI; This BB17 CDNA library was generated by  
subtraction of the BB16 library with 4000 previously  
sequenced clones. The BB16 library was contributed by the  
Soares laboratory and it was constructed and normalized  
as described by Bonaldo, M.F., Lennon, G. and Soares,  
M.B. (1996), Genome Research 6(9): 791-806. RNA was  
prepared from dissected brains of adult worker bees of  
various ages and various behavioral groups."

BASE COUNT 99 a 100 c 104 g 110 t 1 others  
ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 414;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CGAAGCTTCGAGAT 18  
|||||  
164 CGAAGCTTCGAGAT 177

RESULT 17 424 bp mRNA linear EST 11-MAR-2003  
CB333691 TGESTzyf67b10.y1 TGME49 B7 Tachyzoite CDNA Library 2 Toxoplasma  
LOCUS gondii CDNA clone TGESTzyf67b10.y1 5', mRNA sequence.  
DEFINITION  
ACCESSION CB333691  
VERSION CB333691.1 GI:28915374  
KEYWORDS EST.  
SOURCE Toxoplasma gondii  
ORGANISM Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
Sarcocystidae; Toxoplasma.  
1 (bases 1 to 424)  
Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajlaka, J.A., White, M.,  
Clifton, S., Page, D., Martin, J., Wylie, T., Dante, M., Marra, M.,  
Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter,  
E., Bennett, J., Franklin, C., Tsagaris, R., Ronko, I., Kennedy,  
S., Maguire, L., Waterston, R. and Wilson, R.  
Toxoplasma EST Project  
Unpublished  
Contact: Clifton, S.  
Toxoplasma EST Project  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: toxo@wustl.wustl.edu  
Contact David Sibley (toxos@borcim.wustl.edu) for further  
information relating to organism, libraries, or clone availability.  
Seq primer: -40R from Gibco.  
Location/Qualifiers  
1. 424  
/organism="Toxoplasma gondii"  
/mol\_type="mRNA"  
/db\_xref="taxon:5811"  
/clone="TGESTzyf67b10.y1"  
/dev\_stage="Tachyzoite"  
/lab\_host="E.coli XL10"  
/note="Vector: pBluescript II SK+; Site 1: XhoI; Site 2:  
EcotRI; The CDNA library was constructed by Kelang Tang,  
and Robert Cole at Washington University. CDNA was  
synthesized from poly mRNA using an oligo-dT primer  
containing a XhoI site. Following second strand synthesis,  
EcotRI adapters were ligated to the CDNA, and products were  
size-selected on sephacryl S500. The CDNA were  
directionally cloned into the EcotRI/XhoI prepared  
pBluescript II SK+ vector, and transformed into XL10 cells  
(Stratagene). The library may contain a small percentage  
of host or bacterial contaminants."

FEATURES  
source

BASE COUNT 93 a 128 c 103 g 100 t



Tel: 314 286 1800  
Fax: 314 286 1810

Email: [est@watson.wustl.edu](mailto:est@watson.wustl.edu)  
Library was constructed by H. Bode and B. Blumberg DNA sequencing  
by: Washington University Genome Sequencing Center For information  
on obtaining a clone please contact: Hans Bode ([hnbode@uci.edu](mailto:hnbode@uci.edu))  
Seq primer: Primer name ambiguous  
High quality sequence stop: 426.  
Location/Qualifiers

# FEATURES

source

1..466

/organism="Hydra magnipapillata"

/mol\_type="mRNA"

/db\_xref="taxon:6085"

/lab\_host="Hydra CDNA library"

/clone\_lib="Hydra CDNA library"

/note=Vector: pSPORT6; Site 1: NotI; Site 2: SalI;

libraries prepared by Phil Wigge, Plant Molecular and

Cellular Biology, Lab (Detlev Meigel), The Salk Institute

for Biological Science, 10010 North Torrey Pines Road, La

Jolla, CA 92037."

# BASE COUNT

144 a 82 c 73 g 167 t

# ORIGIN

Query Match 66.7%; Score 14; DB 14; Length 466;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AACGTTCCGAGATGA 20

Db 106 AACGTTCCGAGATGA 93

# RESULT 21

LOCUS

DEFINITION

CNS09GNZ 469 bp mRNA linear HTC 08-JAN-2003

Single read from an extremity of a full-length cDNA clone made from

Anopheles gambiae total adult females. 5-PRIME end of clone

FK0AC37DA02 of strain 6-9 of Anopheles gambiae (African malaria

mosquito).

ACCESSION BX057675.1 GI:27630956

VERSION HTG

KEYWORDS

SOURCE

ORGANISM

Anopheles gambiae (African malaria mosquito)

Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;

Anopheles.

1 (bases 1 to 469)

REFERENCE

Genoscope.

Direct Submission

Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr))

- Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)

Location/Qualifiers

1..469

/organism="Anopheles gambiae"

/mol\_type="mRNA"

/strain="6-9"

/db\_xref="taxon:7165"

/clone="FK0AC37DA02"

/plasmid="pME18S-FU"

/note="end : 5-PRIME"

BASE COUNT 115 a 126 c 157 g 71 t

ORIGIN

Query Match 66.7%; Score 14; DB 11; Length 469;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTGAACGTTG 14

Db 214 TCGTGAACGTTG 201

# RESULT 22

AA097939

LOCUS

DEFINITION

AA097939 484 bp mRNA linear EST 15-FEB-1997

mus2901.r1 Stragene mouse Tcell 937311 Mus musculus cDNA clone

IMAGE:550608 5' similar to gb:X69392.608 RIBOSOMAL PROTEIN L26

(HUMAN); gb:X80699 M.musculus L26 mRNA (MOUSE);, mRNA sequence.

ACCESSION

AA097939

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

(house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 484)

REFERENCE

AUTHORS

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HMI Mouse EST Project

Unpublished

CONTACT: Marra M/Mouse EST Project

Washington University School of Medicine

444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: [mouseest@watson.wustl.edu](mailto:mouseest@watson.wustl.edu)

This clone is available royalty-free through LNL; contact the

IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

WGI:331400

Seq primer: -28m13 rev1 ET from Amerham

High quality sequence stop: 7.

Location/Qualifiers

1..484

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/clone="IMAGE:550608"

/tissue\_type="Tcell"

/dev\_stage="M30 CD4+ cells"

/lab\_host="SOAR (kanamycin resistant)"

/clone\_lib="Stragene mouse Tcell 937311"

/note=Organ: blood; Vector: pBluescript SK-; Site 1:

ECORI; Site 2: XhoI; Vector: pBluescript SK-; Primer:

Oligo dr. M30 CD4+ cells. Average insert size: 1.0 kb;

Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTGGCGCGAG

3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

BASE COUNT 142 a 128 c 115 g 99 t

ORIGIN

Query Match 66.7%; Score 14; DB 9; Length 484;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACGTTCGAGATGAT 21

Db 424 ACGTTCGAGATGAT 437

# RESULT 23

BM636144

LOCUS

DEFINITION

BM636144 486 bp mRNA linear EST 26-FEB-2002

17000687561542 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone

IMAGE:550608 5' similar to gb:X69392.608 RIBOSOMAL PROTEIN L26

(HUMAN); gb:X80699 M.musculus L26 mRNA (MOUSE);, mRNA sequence.

ACCESSION

BM636144

VERSION

KEYWORDS

SOURCE

ORGANISM

Anopheles gambiae (African malaria mosquito)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;



REFERENCE 1 (bases 1 to 486)  
 AUTHORS Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab  
 TITLE R., Collins, F.H., Venter, J.C. and Hoffman, S.L.  
 JOURNAL Celera Anopheles gambiae EST project  
 COMMENT Unpublished  
 CONTACT: Holt R.A.  
 Celera Genomics  
 45 W. Gude Dr., Rockville, MD 20850, USA  
 Tel: 2404533151  
 Fax: 2404534580  
 Email: HoltR@celera.com  
 Plate: NU01004922 row: N column: 16  
 Seq primer: M13 Reverse.

## FEATURES

source

Location/Qualifiers

1..486  
 /organism="Anopheles gambiae"  
 /mol\_type="mRNA"  
 /strain="RSP-ST (Reduced susc. to Permethrin - std.  
 chromosome)"  
 /db\_xref="taxon:7165"  
 /clone="19600449644818"  
 /dev\_stage="Adult"  
 /lab\_host="DHI10b"  
 /clone\_1ib="A.Gam.ad.cDNA1"  
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole  
 adult mosquitoes (mixed sex) frozen on liquid nitrogen.  
 cDNA inserts >500 bp cloned directionally into pSport 1.  
 Not 1 site is 3'. Clones available through the Malaria  
 Research and Reference Reagent Resource Center  
 (www.malaria.mr4.org)."  
 BASE COUNT 119 a 129 c 156 g 82 t  
 ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 486;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGCTTCGAGAT 18  
 |||||  
 Db 387 CGAAGCTTCGAGAT 374

RESULT 24  
 BM652631/c 492 bp mRNA linear EST 26-FEB-2002  
 LOCUS 17000687313490 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
 DEFINITION 19600449634767 5', mRNA sequence.  
 ACCESSION BM652631  
 VERSION BM652631.1 GI:18952142  
 KEYWORDS EST.  
 SOURCE Anopheles gambiae (African malaria mosquito)  
 ORGANISM Anopheles gambiae  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
 Anophelinae  
 1 (bases 1 to 492)  
 Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab  
 R., Collins, F.H., Venter, J.C. and Hoffman, S.L.  
 TITLE Celera Anopheles gambiae EST project  
 JOURNAL Unpublished  
 COMMENT Contact: Holt R.A.  
 Celera Genomics  
 45 W. Gude Dr., Rockville, MD 20850, USA  
 Tel: 2404533151  
 Fax: 2404534580  
 Email: HoltR@celera.com  
 Plate: NU01004922 row: K column: 21  
 Seq primer: M13 Reverse.

## FEATURES

source

Location/Qualifiers

1..492  
 /organism="Anopheles gambiae"  
 /mol\_type="mRNA"

## BASE COUNT

117 a 134 c 157 g 84 t

Query Match 66.7%; Score 14; DB 12; Length 492;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGCTTCGAGAT 18  
 |||||  
 Db 440 CGAAGCTTCGAGAT 427

RESULT 25  
 BM644091/c 493 bp mRNA linear EST 26-FEB-2002  
 LOCUS 17000687313490 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
 DEFINITION 19600449671469 5', mRNA sequence.  
 ACCESSION BM644091  
 VERSION BM644091.1 GI:18943602  
 KEYWORDS EST.  
 SOURCE Anopheles gambiae (African malaria mosquito)  
 ORGANISM Anopheles gambiae  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
 Anophelinae  
 1 (bases 1 to 493)  
 Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab  
 R., Collins, F.H., Venter, J.C. and Hoffman, S.L.  
 TITLE Celera Anopheles gambiae EST project  
 JOURNAL Unpublished  
 COMMENT Contact: Holt R.A.  
 Celera Genomics  
 45 W. Gude Dr., Rockville, MD 20850, USA  
 Tel: 2404533151  
 Fax: 2404534580  
 Email: HoltR@celera.com  
 Plate: NU01004922 row: E column: 03  
 Seq primer: M13 Reverse.

## FEATURES

source

Location/Qualifiers

1..493  
 /organism="Anopheles gambiae"  
 /mol\_type="mRNA"  
 /strain="RSP-ST (Reduced susc. to Permethrin - std.  
 chromosome)"  
 /db\_xref="taxon:7165"  
 /clone="19600449671469"  
 /dev\_stage="Adult"  
 /lab\_host="DHI10b"  
 /clone\_1ib="A.Gam.ad.cDNA1"  
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole  
 adult mosquitoes (mixed sex) frozen on liquid nitrogen.  
 cDNA inserts >500 bp cloned directionally into pSport 1.  
 Not 1 site is 3'. Clones available through the Malaria  
 Research and Reference Reagent Resource Center  
 (www.malaria.mr4.org)."  
 BASE COUNT 120 a 129 c 159 g 85 t  
 ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 493;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 CGAAGCTTCGAGAT 18  
 |||||  
 Db 398 CGAAGCTTCGAGAT 385

RESULT 26  
 BM597612/c 499 bp mRNA linear EST 25-FEB-2002  
 LOCUS 17000687499086 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone  
 DEFINITION 19600449683979 5', mRNA sequence.

ACCESSION BM597612  
 VERSION BM597612.1 GI:18895703  
 KEYWORDS EST

SOURCE Anopheles gambiae (African malaria mosquito)  
 ORGANISM Anopheles gambiae

REFERENCE BUKARYOTA; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.

AUTHORS Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.

TITLE Celera Anopheles gambiae EST project  
 JOURNAL Unpublished

COMMENT Contact: Holt R.A.  
 Celera Genomics  
 45 W. Gude Dr., Rockville, MD 20850, USA  
 Tel: 2404533151  
 Fax: 2404534580  
 Email: HoltR@celera.com  
 Plate: NU01004B2S row: M column: 21  
 Seq primer: M13 Reverse.

FEATURES  
 source 1..499  
 location/Qualifiers

/organism="Anopheles gambiae"  
 /mol\_type="mRNA"  
 /strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"  
 /db\_xref="taxon:7165"  
 /clone="19600449683979"  
 /dev\_stage="Adult"  
 /lab\_host="DH10b"  
 /clone\_11b="A.Gam.ad.cDNA.blood1"  
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'.

Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)"  
 BASE COUNT 121 a 131 c 159 g 88 t  
 ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 499;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 CGAAGCTTCGAGAT 18  
 |||||  
 Db 428 CGAAGCTTCGAGAT 415

RESULT 27  
 BM611518/c 504 bp mRNA linear EST 25-FEB-2002  
 LOCUS 17000687115945 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone  
 DEFINITION 19600449722493 5', mRNA sequence.

ACCESSION BM611518  
 VERSION BM611518.1 GI:18909622  
 KEYWORDS EST

SOURCE Anopheles gambiae (African malaria mosquito)  
 ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.

REFERENCE 1 (bases 1 to 504)  
 Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.

TITLE Celera Anopheles gambiae EST project  
 JOURNAL Unpublished

COMMENT Contact: Holt R.A.  
 Celera Genomics  
 45 W. Gude Dr., Rockville, MD 20850, USA  
 Tel: 2404533151  
 Fax: 2404534580  
 Email: HoltR@celera.com  
 Plate: NU01004A9Y row: B column: 15  
 Seq primer: M13 Reverse.

FEATURES  
 source 1..504  
 location/Qualifiers

/organism="Anopheles gambiae"  
 /mol\_type="mRNA"  
 /strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"  
 /db\_xref="taxon:7165"  
 /clone="19600449722493"  
 /dev\_stage="Adult"  
 /lab\_host="DH10b"  
 /clone\_11b="A.Gam.ad.cDNA.blood1"  
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'.

Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)"  
 BASE COUNT 123 a 132 c 161 g 88 t  
 ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 504;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 CGAAGCTTCGAGAT 18  
 |||||  
 Db 426 CGAAGCTTCGAGAT 413

RESULT 28  
 BM866297 512 bp mRNA linear EST 06-MAY-2003  
 LOCUS mgc8005x24f.b Magnaporthe grisea CS Uni-Zap XR library Magnaporthe grisea cDNA clone mgc8005x24 5', mRNA sequence.

ACCESSION BM866297  
 VERSION BM866297.2 GI:30394811  
 KEYWORDS EST

SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)  
 ORGANISM Magnaporthe grisea

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.

1 (bases 1 to 512)  
 Ebbole, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G., Bhatterai, K. and Dean, R.A.

TITLE Expressed sequence tags from the rice blast fungus, Magnaporthe grisea  
 JOURNAL Unpublished  
 COMMENT On Mar 7, 2002 this sequence version replaced gi:19233979.

Contact: Ebbole DJ  
 Department of Plant Pathology & Microbiology  
 Texas A&M University  
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA

Tel: 979 845 4831  
 Fax: 979 845 6483  
 Email: d-ebbole@tamu.edu

Chromatogram file of this sequence is available, see contact person  
 Chromatogram hit (April. 22, 2003) gb|EAA28529.1| hypothetical protein  
 [Neurospora crassa] 107 9e-49

PCR Primers  
 FORWARD: T3 primer  
 BACKWARD: T7 primer  
 Plate: mgc805 row: E column: 24  
 Seq primer: T3.  
 Location/Qualifiers  
 1..512

FEATURES  
 source  
 /organism="Magnaporthe grisea"  
 /mol\_type="mRNA"  
 /strain="Guy11"  
 /db\_xref="taxon:148305"  
 /clone="mgc805x24"  
 /sex="Mati-2 hermaphrodite"  
 /cell\_type="conidia"  
 /clone\_lib="Magnaporthe grisea CS Uni-Zap XR Library"  
 /note="Vector: pBluescriptSK-, Site\_1: EcoRI, Site\_2: XhoI  
 ; unidirectional cloning. EcoRI site has T3 primer and  
 predominantly 5' reads. T7 primer on XhoI side of insert.  
 Conidia library. Point inoculation of Guy11 at center of  
 oatmeal agar plate. Conidia were harvested after two weeks  
 of growth. Sequences were processed by one of two methods.  
 where a full-length alignment to the M. grisea genome  
 sequence was available, the EST sequence was trimmed  
 according to the alignment, otherwise sequence quality was  
 assessed using phredphrap version 991019 and trimmed  
 according to phd files (0.05) and for vector seqs."  
 BASE COUNT 118 a 161 c 119 g 114 t  
 ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 512;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AACGTTCCAGATGA 20  
 |||||  
 356 AACGTTCCAGATGA 369

RESULT 29  
 LOCUS CB358730 513 bp mRNA linear EST 17-MAR-2003  
 DEFINITION ZF001-P00024-DPE-F-A G12 GISZF001 Dario rerio cDNA clone  
 IMAGE:5900672 5' similar to fc24g12.y1 Zebrafish Washu WRMG EST  
 Dario rerio cDNA clone IMAGE:3722374 5' mRNA sequence.  
 CB358730  
 ACCESSION CB358730.1 GI:29001661  
 VERSIONS  
 KEYWORDS  
 SOURCE Dario rerio (zebrafish)  
 ORGANISM Dario rerio

REFERENCE  
 AUTHORS Mathavan,S., Wei,C., Thoreau,H., Chia,J.M. and Ruan,Y.  
 TITLE Mathavan,S., Wei,C., Thoreau,H., Chia,J.M. and Ruan,Y.  
 JOURNAL Genome Institute of Singapore, Zebrafish EST Collection  
 COMMENT Unpublished  
 Contact: Ruan Y  
 Laboratory of Molecular Biotechnology  
 Genome Institute of Singapore  
 1 Science Park Road, The Capricorn #05-01, Singapore 117528  
 Tel: +65 6827 5200  
 Fax: +65 6827 5201  
 Email: g1ery@nus.edu.sg  
 GIS Clone ID: ZF001-P00024-PP\_M23  
 PCR Primers  
 FORWARD: M13  
 BACKWARD: M13  
 Plate: ZF001-P00024-DPE-F-A  
 Seq primer: CCGCATTAAGTGTATAGCA  
 High quality sequence stop: 513.  
 Location/Qualifiers  
 1..513  
 /organism="Dario rerio"

FEATURES  
 source  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7955"  
 /clone="IMAGE:6900672"  
 /tissue\_type="Embryo"  
 /dev\_stage="7 Different embryonic Stages (From just  
 fertilized Embryos to 72 hours just hatched baby fish)"  
 /lab\_host="DH10B"  
 /clone\_lib="GISZF001"  
 /note="Vector: pDMR-LIB, Site\_1: Sfi A (GGCCATTACGGCC);  
 Site\_2: Sfi B (GGCCGCTCGGCC); Priming method: Sfi-(dT)30  
 primed; Priming sequence: 5'-ATTCTAGA GGCCGAGCGGCC  
 GACATG(T)30VN; Directionally cloned, 5' cloning site:  
 Sfi A site GGCCATTACGGCC; 5' linker/adaptor sequence:  
 5'-AGCAGTGGATCAACGACGAGTGGCC; 3' cloning site: Sfi B  
 site GGCCGCTCGGCC; 3' linker/adaptor sequence: same  
 as the priming sequence; Average insert size: 2kb; For  
 PCR insert analysis: Use M13 forward and reverse primers;  
 Library Amplified Recombinants (inserts): 984; Library  
 complexity: 5x10<sup>6</sup>; Full-length construction (method):  
 SMART, a Clontech method; Library constructed by: S.  
 Mathavan, Chia-Lin Wei, and Yijun Ruan Genome Institute of  
 Singapore"  
 BASE COUNT 131 a 108 c 112 g 162 t  
 ORIGIN

Query Match 66.7%; Score 14; DB 14; Length 513;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AACGTTCCAGATGA 20  
 |||||  
 422 AACGTTCCAGATGA 435

RESULT 30  
 LOCUS BH899325 521 bp DNA linear GSS 30-AUG-2002  
 DEFINITION Ota00392 Ostreococcus tauri genomic shotgun library Ostreococcus  
 tauri genomic clone ota23a09.b 5', genomic survey sequence.  
 BH899325  
 ACCESSION BH899325.1 GI:22550820  
 VERSIONS  
 KEYWORDS  
 SOURCE GSS.  
 ORGANISM Ostreococcus tauri

REFERENCE  
 AUTHORS Derelle,E., Ferraz,C., Lagoda,P., Eychenne,S., Cooke,R., Regad,F.,  
 Moreau,H., Courties,C., Delseny,M., Demaille,J., Picard,A. and  
 Moreau,H.  
 TITLE DNA libraries for sequencing the genome of Ostreococcus tauri  
 (Chlorophytae, Prasinophyceae): the smallest free-living eukaryotic  
 cell  
 J. Phycol. 38 (6), 1150-1156 (2002)  
 CONTACT: Moreau H  
 Laboratoire Arago  
 CNRS UMR 7628  
 BP 44, Avenue Fontaule, 66651 Banyuls sur mer, France  
 Tel: (33)468887309  
 Fax: (33)468887398  
 Email: h.moreau@obs-banyuls.fr  
 Seq primer: forward  
 Class: Shotgun.  
 Location/Qualifiers  
 1..521  
 /organism="Ostreococcus tauri"  
 /mol\_type="genomic DNA"  
 /strain="OTTH0595"  
 /db\_xref="taxon:70448"  
 /clone="ota23a09.b"  
 /clone\_lib="Ostreococcus tauri genomic shotgun library"  
 /note="Vector: Bluescript; Site 1: EcoRV; Site 2: EcoRV;  
 Shotgun library prepared after ionization of the genomic

DNA. Blunt ligation in EcoRV site of Bluescript. Size selection of the inserts after agarose electrophoresis between 1 and 3 kb."

BASE COUNT 84 a 146 c 214 g 77 t

Query Match 66.7%; Score 14; DB 28; Length 521;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGTCGACGTTGCA 15  
|||||  
Db 77 CGTCGACGTTGCA 90

RESULT 31  
LOCUS BM618536/c 527 bp mRNA linear EST 25-FEB-2002  
DEFINITION 17000687439164 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
19600449662307 5', mRNA sequence.

ACCESSION BM618536  
VERSION BM618536.1 GI:18916954  
KEYWORDS EST.  
SOURCE Anopheles gambiae (African malaria mosquito)  
ORGANISM Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.

REFERENCE 1 (bases 1 to 527)  
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab  
R., Collins,F.H., Venter,J.C. and Hoffman,S.L.  
Celera Anopheles gambiae EST project  
Unpublished  
Contact: Holt R.A.  
Celera Genomics  
45 W. Gude Dr., Rockville, MD 20850, USA  
Tel: 2404533151  
Fax: 2404534580  
Email: HoltRA@celera.com  
Plate: NU01004185 row: G column: 09  
Seq primer: M13 Reverse

# FEATURES

## source

1..527  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="RSP-ST (Reduced susc. to Permethrin - std.  
chromosome)"  
/db\_xref="taxon:7165"  
/clone="19600449662307"  
/dev\_stage="Adult"  
/lab\_host="DH10b"  
/clone\_1lb="A.Gam.ad.cDNA1"  
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole  
adult mosquitoes (mixed sex) frozen on liquid nitrogen.  
cDNA inserts >500 bp cloned directionally into pSport 1.  
Not 1 site is 3'. Clones available through the Malaria  
Research and Reference Reagent Resource Center  
(www.malaria.mr4.org)."

BASE COUNT 125 a 138 c 174 g 90 t

## ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 527;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACGTTGAGAT 18  
|||||  
Db 450 CGACGTTGAGAT 437

RESULT 32  
LOCUS BM618261/c 528 bp mRNA linear EST 25-FEB-2002

DEFINITION 17000687437986 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
19600449620529 5', mRNA sequence.

ACCESSION BM618261  
VERSION BM618261.1 GI:18916553  
KEYWORDS EST.  
SOURCE Anopheles gambiae (African malaria mosquito)  
ORGANISM Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.

REFERENCE 1 (bases 1 to 528)  
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab  
R., Collins,F.H., Venter,J.C. and Hoffman,S.L.  
Celera Anopheles gambiae EST project  
Unpublished  
Contact: Holt R.A.  
Celera Genomics  
45 W. Gude Dr., Rockville, MD 20850, USA  
Tel: 2404533151  
Fax: 2404534580  
Email: HoltRA@celera.com  
Plate: NU01004NAK row: J column: 15  
Seq primer: M13 Reverse

# FEATURES

## source

1..528  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="RSP-ST (Reduced susc. to Permethrin - std.  
chromosome)"  
/db\_xref="taxon:7165"  
/clone="19600449620529"  
/dev\_stage="Adult"  
/lab\_host="DH10b"  
/clone\_1lb="A.Gam.ad.cDNA1"  
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole  
adult mosquitoes (mixed sex) frozen on liquid nitrogen.  
cDNA inserts >500 bp cloned directionally into pSport 1.  
Not 1 site is 3'. Clones available through the Malaria  
Research and Reference Reagent Resource Center  
(www.malaria.mr4.org)."

BASE COUNT 127 a 141 c 168 g 92 t

## ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 528;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACGTTGAGAT 18  
|||||  
Db 438 CGACGTTGAGAT 425

RESULT 33  
LOCUS BM632494/c 528 bp mRNA linear EST 26-FEB-2002  
DEFINITION 17000687504372 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
19600449666961 5', mRNA sequence.

ACCESSION BM632494  
VERSION BM632494.1 GI:18932005  
KEYWORDS EST.  
SOURCE Anopheles gambiae (African malaria mosquito)  
ORGANISM Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.

REFERENCE 1 (bases 1 to 528)  
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab  
R., Collins,F.H., Venter,J.C. and Hoffman,S.L.  
Celera Anopheles gambiae EST project  
Unpublished  
Contact: Holt R.A.  
Celera Genomics  
45 W. Gude Dr., Rockville, MD 20850, USA

RESULT 34  
LOCUS BM618261/c 528 bp mRNA linear EST 25-FEB-2002

Tel: 2404533151  
 Fax: 2404534580  
 Email: HoltRA@celera.com  
 Plate: NU01004HMK row: I column: 07  
 Seq primer: M13 Reverse.  
 Location/Qualifiers

FEATURES  
 source  
 1..528  
 /organism="Anopheles gambiae"  
 /mol\_type="mRNA"  
 /strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"  
 /db\_xref="taxon:7165"  
 /clone="19600449617956"  
 /dev\_stage="Adult"  
 /lab\_host="DHI10b"  
 /clone\_lib="A.Gam.ad.cDNA1"  
 /note="Vector: pSport1; Site\_1: SalI; Site\_2: NotI; whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."  
 BASE COUNT 123 a 136 c 168 g 101 t  
 ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 528;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGAAGCTTCGAGAT 18  
 |||||  
 Db 468 CGAAGCTTCGAGAT 455

RESULT 34 528 bp DNA linear GSS 13-DEC-2000  
 LOCUS TA99D10P  
 DEFINITION T. brucei sheared genomic DNA clone 99d10, forward sequence,  
 genomic survey sequence.  
 ACCESSION AL460276 GI:11862154  
 VERSION AL460276  
 KEYWORDS GSS.  
 SOURCE Trypanosoma brucei  
 ORGANISM Trypanosoma brucei  
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.  
 1 (bases 1 to 528)  
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
 Melville, S.E., Rajandream, M.A. and Barrett, B.G.  
 Direct Submission  
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
 nh@sanger.ac.uk  
 nh@sanger.ac.uk  
 Constructed at the Institute for Genomic Research (TIGR),  
 Rockville, MD. Genomic DNA isolated from a cloned population of  
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
 to give a tight size distribution (4 kb). The v + i method used for the library construction is  
 described in detail in Smith, H. and Venter, J.C. (Making small  
 insert libraries for whole genome shotgun sequencing projects. In  
 Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.  
 Barrell, Oxford University Press, 1999).  
 Email: nelsayed@tigr.org  
 Details of T. brucei sequencing at the Sanger Centre are available  
 at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).  
 Location/Qualifiers

FEATURES  
 source  
 1..528  
 /organism="Trypanosoma brucei"  
 /mol\_type="genomic DNA"  
 /strain="TREU927"  
 /db\_xref="taxon:5691"

BASE COUNT 116 a 177 c 118 g 117 t  
 ORIGIN

Query Match 66.7%; Score 14; DB 29; Length 528;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAAGCTTCG 14  
 |||||  
 Db 29 TCGTCGAAGCTTCG 42

RESULT 35 533 bp mRNA linear EST 26-FEB-2002  
 LOCUS BM641866/c  
 DEFINITION 17000687308831 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
 19600449617956 5', mRNA sequence.  
 ACCESSION BM641866  
 VERSION BM641866.1 GI:18941377  
 KEYWORDS EST.  
 SOURCE Anopheles gambiae (African malaria mosquito)  
 ORGANISM Anopheles gambiae  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
 Anopheles.  
 1 (bases 1 to 533)  
 Holt, R.A., Lin, D.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab  
 , R., Collins, F.H., Venter, J.C. and Hoffman, S.L.  
 Celera Anopheles gambiae EST project  
 Unpublished  
 Contact: Holt R.A.  
 Celera Genomics  
 45 W. Gude Dr., Rockville, MD 20850, USA  
 Tel: 2404533151  
 Fax: 2404534580  
 Email: HoltRA@celera.com  
 Plate: NU01004HMK row: O column: 10  
 Seq primer: M13 Reverse.  
 Location/Qualifiers

FEATURES  
 source  
 1..533  
 /organism="Anopheles gambiae"  
 /mol\_type="mRNA"  
 /strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"  
 /db\_xref="taxon:7165"  
 /clone="19600449617956"  
 /dev\_stage="Adult"  
 /lab\_host="DHI10b"  
 /clone\_lib="A.Gam.ad.cDNA1"  
 /note="Vector: pSport1; Site\_1: SalI; Site\_2: NotI; whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."  
 BASE COUNT 139 a 147 c 173 g 74 t  
 ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 533;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGAAGCTTCGAGAT 18  
 |||||  
 Db 336 CGAAGCTTCGAGAT 323

RESULT 36 534 bp DNA linear GSS 17-MAR-1999  
 LOCUS AQ407920  
 DEFINITION HS 5055\_B2 E08 T7A RPC1-11 Human Male BAC Library Homo sapiens  
 genomic clone Plate=631 Col=16 Row=J, genomic survey sequence.

ACCESSION	AA0407920	GI:4427459	
VERSION	AA0407920.1		
KEYWORDS	GSS.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.		
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)		
MEDLINE	99380589		
PUBMED	10449764		
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel.: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@djong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsg.washington.edu Plate: 631 row: J column: 16 Seg primer: T7 Class: BAC ends High quality sequence stop: 534. Location/Qualifiers 1..534 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone="Plate=631 Col=16 Row=J" /sex="male" /clone_lib="RPCI-11 Human Male BAC library" /note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"		
BASE COUNT	173 a 71 c 149 g 135 t 6 others		
ORIGIN			
Query Match	66.7%;	Score 14;	DB 28; Length 534;
Best Local Similarity	100.0%;	Pred. No. 3.2e+02;	
Matches	14; Conservative	0; Mismatches	0; Indels 0; Gaps 0;
CY	7 AACGTCGAGATGA 20		
Db	150 AACGTCGAGATGA 163		
RESULT 37			
AL695492/c	AL695492	541 bp	mRNA linear EST 21-MAR-2002
LOCUS	AL695492	NAP1 Anopheles gambiae	CDNA NAP1-P31-H-11-5, mRNA
DEFINITION	Sequence.		
ACCESSION	AL695492		
VERSION	AL695492.1	GI:19615134	
KEYWORDS	EST.		
SOURCE	Anopheles gambiae (African malaria mosquito)		
ORGANISM	Anopheles gambiae		
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anophelae.		
AUTHORS	1 (bases 1 to 541)		
Christophides,G.K., Blasg,K., Zdobnov,E.M., Carmouche,R., Benes,V.			

and Kafatos, P.C.  
Anopheles gambiae EST, European Molecular Biology Laboratory  
JOURNAL  
COMMENT  
Unpublished  
Contact: Christophides GK  
Fotis C. Kafatos Laboratory  
European Molecular Biology Laboratory  
Meyerhofstrasse 1, 69117 Heidelberg, Germany  
Tel: +49 6221 387-440  
Fax: +49 6221 387-306  
Email: christophe.mbl-heidelberg.de  
Plate: F31 row: H column: 11.  
Location/Qualifiers  
1. 541  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/db\_xref="taxon:7165"  
/clone="NAP1-P31-H-11-5"  
/lab\_host="E. coli DH10B"  
/clone\_lib="NAP1"  
/note="Vector: pRT3D-Pac (Pharmacia); Site 1: NotI;  
Site 2: EcoRI; ESTs sequenced from the T7 priming site  
that reads from the 5' end of cDNA. The NAP1 is a  
directionally cloned and normalized, oligo-T primed cDNA  
library constructed from a mixture of Anopheles gambiae  
developmental stages according to: Bonaldo, Lemon &  
Soares (1996): Normalization and Subcloning: Two  
Approaches To Facilitate Gene Discovery, Genome Research  
6, 791-806."

BASE COUNT 134 a 134 c 175 g 96 t 2 others  
ORIGIN

Query Match 66.7%; Score 14; DB 9; Length 541;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY 5 CGAACGTTCCGAGAT 18  
|||||  
Db 405 CGAACGTTCCGAGAT 392

RESULT 38  
BI511012/c  
LOCUS  
DEFINITION B1610004.20EB05.5 Bee Brain Normalized Library, B16 Apis mellifera  
VERSION  
ACCESSION B1511012  
KEYWORDS  
SOURCE B1511012.1 GI:15361386  
ORGANISM  
EST.  
Apis mellifera (honeybee)  
Apis mellifera  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;  
Apidae; Apis.  
1 (bases 1 to 544)  
Whitfield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L.,  
Pardinas, J., Robertson, H.M., Soares, B. and Robinson, G.B.  
Annotated expressed sequence tags and cDNA microarrays for studies  
of brain and behavior in the honey bee  
Genome Res. 12 (4), 555-566 (2002)  
21929762  
11932240  
Contact: Gene E. Robinson  
Department of Entomology  
University of Illinois  
505 S. Goodwin Ave., Urbana, IL 61801, USA  
Tel: 217 265 0309  
Fax: 217 244 3499  
Email: genrob@life.uiuc.edu  
This research was funded by the University of Illinois Critical  
Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation  
Award in Functional Genomics to G.E. Robinson and an NSF  
Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.  
PCR Primers

FORWARD: TAATACGACTCATAATAGG  
 BACKWARD: ATTAACTCTACTAAG  
 Plate: BB160004A20 row: E column: 05  
 Seq primer: AGCGATTAACATTTCACACAGAA  
 High quality sequence stop: 544.  
 Location/Qualifiers

FEATURES  
 source  
 1..544  
 /organism="Apis mellifera"  
 /mol\_type="mRNA"  
 /strain="mixed strains of European bees, predominantly A.m. ligustica"  
 /db\_xref="taxon:7460"  
 /clone="BB160004A20E05"  
 /sex="female"  
 /tissue\_type="brain"  
 /dev\_stage="adult worker honey bee"  
 /lab\_host="DH10B"  
 /clone\_lib="Bee Brain Normalized Library, BB16"  
 /note="Organ: brain; Vector: pRTT3-Pac; Site 1: EcorI; Site 2: NotI; The BB16 library was contributed by the Soars laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soars, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from dissected brains of adult worker bees of various ages and various behavioral groups. "  
 BASE COUNT 119 a 147 c 143 g 135 t  
 ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 544;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGTCGACGCTTCGA 15  
 |||||  
 132 CGTCGACGCTTCGA 119

RESULT 39  
 BM649585/c 546 bp mRNA linear EST 26-FEB-2002  
 LOCUS 17000687369108 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
 DEFINITION 19600449617798 5', mRNA sequence.  
 ACCESSION BM649585  
 VERSION BM649585.1 GI:18949096  
 KEYWORDS EST  
 SOURCE Anopheles gambiae (African malaria mosquito)  
 ORGANISM Anopheles gambiae  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.  
 1 (bases 1 to 546)  
 Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab  
 R., Collins,F.H., Venter,J.C. and Hoffman,S.L.  
 Celera Anopheles gambiae EST project  
 Unpublished  
 Contact: Holt R.A.  
 Celera Genomics  
 45 W. Gude Dr., Rockville, MD 20850, USA  
 Tel: 2404533151  
 Fax: 2404534580  
 Email: HoltRA@celera.com  
 Plate: NU01004N8E row: H column: 20  
 Seq primer: M13 Reverse.  
 Location/Qualifiers

FEATURES  
 source  
 1..546  
 /organism="Anopheles gambiae"  
 /mol\_type="mRNA"  
 /strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"  
 /db\_xref="taxon:7165"  
 /clone="19600449617798"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B"

/clone\_lib="A.Gam.ad.cDNA1"  
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."  
 BASE COUNT 132 a 145 c 176 g 93 t  
 ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 546;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGCTTCGAGAT 18  
 |||||  
 409 CGAAGCTTCGAGAT 396

RESULT 40  
 BM650226/c 549 bp mRNA linear EST 26-FEB-2002  
 LOCUS 17000687370552 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
 DEFINITION 19600449640068 5', mRNA sequence.  
 ACCESSION BM650226  
 VERSION BM650226.1 GI:18949737  
 KEYWORDS EST  
 SOURCE Anopheles gambiae (African malaria mosquito)  
 ORGANISM Anopheles gambiae  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.  
 1 (bases 1 to 549)  
 Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab  
 R., Collins,F.H., Venter,J.C. and Hoffman,S.L.  
 Celera Anopheles gambiae EST project  
 Unpublished  
 Contact: Holt R.A.  
 Celera Genomics  
 45 W. Gude Dr., Rockville, MD 20850, USA  
 Tel: 2404533151  
 Fax: 2404534580  
 Email: HoltRA@celera.com  
 Plate: NU01004AY4 row: H column: 18  
 Seq primer: M13 Reverse.  
 Location/Qualifiers

FEATURES  
 source  
 1..549  
 /organism="Anopheles gambiae"  
 /mol\_type="mRNA"  
 /strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"  
 /db\_xref="taxon:7165"  
 /clone="19600449640068"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B"

/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."  
 BASE COUNT 126 a 159 c 183 g 81 t  
 ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 549;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGCTTCGAGAT 18  
 |||||  
 286 CGAAGCTTCGAGAT 273

RESULT 41	BM626834/c	550 bp	mRNA	linear	EST 26-FEB-2002
LOCUS	BM626834				
DEFINITION	17000687496213 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone				
ACCESSION	19600449642604 5', mRNA sequence.				
VERSION	BM626834				
KEYWORDS	BM626834.1 GI:18926345				
SOURCE	EST.				
ORGANISM	Anopheles gambiae (African malaria mosquito)				
	Anopheles gambiae				
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.				
REFERENCE	1 (bases 1 to 550)				
AUTHORS	Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab				
	R., Collins,F.H., Venter,J.C. and Hoffman,S.L.				
TITLE	Celera Anopheles gambiae EST project				
JOURNAL	Unpublished				
COMMENT	Contact: Holt R.A.				
	Celera Genomics				
	45 W. Gude Dr., Rockville, MD 20850, USA				
	Tel: 2404533151				
	Fax: 2404534580				
	Email: HoltR@celera.com				
	Plate: NU01003CY3 row: B column: 10				
	Seq primer: M13 Reverse.				
FEATURES	location/Qualifiers				
SOURCE	1..550				
	/organism="Anopheles gambiae"				
	/mol_type="mRNA"				
	/strain="RSP-SF (Reduced susc. to Permethrin - std.				
	chromosome)"				
	/db_xref="taxon:7165"				
	/clone="19600449642604"				
	/dev_stage="Adult"				
	/lab_host="DH10b"				
	/clone_1fb="A.Gam.ad.cDNA1"				
	/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole				
	adult mosquitoes (mixed sex)_frozen on liquid nitrogen.				
	cDNA inserts >500 bp cloned directionally into pSport 1.				
	Not 1 site is 3'. Clones available through the Malaria				
	Research and Reference Reagent Resource Center				
	(www.malaria.m4.org)"				
BASE COUNT	131 a 151 c 187 g 81 t				
ORIGIN					
Query Match	66.7%; Score 14; DB 12; Length 550;				
Best Local Similarity	100.0%; Pred.No. 3.2e+02;				
Matches	14; Conservative 0; Mismatches 0; Indels 0; Gaps 0.				
OR	5 CGAAGCTTCGAGAT 18				
Db	302 CGAAGCTTCGAGAT 289				
RESULT 42.	BM633500	554 bp	mRNA	linear	EST 26-FEB-2002
LOCUS	17000687507362 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone				
DEFINITION	19600449648215 5', mRNA sequence.				
ACCESSION	BM633500				
VERSION	BM633500.1 GI:18933011				
KEYWORDS	EST.				
SOURCE	Anopheles gambiae (African malaria mosquito)				
ORGANISM	Anopheles gambiae				
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.				
REFERENCE	1 (bases 1 to 554)				
AUTHORS	Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab				
	R., Collins,F.H., Venter,J.C. and Hoffman,S.L.				
TITLE	Celera Anopheles gambiae EST project				

```

JOURNAL-      Unpublished
COMMENT       Contact: Holt R.A.
              Celera Genomics
              45 W. Gude Dr., Rockville, MD 20850, USA
              Tel.: 2404533151
              Fax: 2404534580
              Email: HOLTRA@celera.com
              Plate: NT010049M5 row: L column: 05
              Seq primer: M13 Reverse.

FEATURES
source        Location/Qualifiers
              1..554
                /organism="Anopheles gambiae"
                /mol_type="mRNA"
                /strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
                /db_xref="taxon:7165"
                /clone="19600449648215"
                /dev_stage="Adult"
                /lab_host="DH10b"
                /clone_lib="A.Gam.ad.cDNA1"
                /note="Vector: pSPori; Site_1: SalI, Site_2: NotI; whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
```



/clone="otdb0609.b"  
 /note="Vector: Bluescript; Site 1: EcoRV; Site 2: EcoRV;  
 Shotgun library prepared after sonication of the genomic  
 DNA. Blunt ligation in EcoRV site of Bluescript. Size  
 selection of the inserts after agarose electrophoresis  
 between 1 and 3 kb."  
 BASE COUNT 129 a 142 c 174 g 111 t  
 ORIGIN

Query Match 66.7%; Score 14; DB 28; Length 556;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTGAACGTTTCG 14  
 |||||  
 Db 254 TCGTGAACGTTTCG 241

RESULT 44  
 A2216899 558 bp DNA linear GSS 09-JUN-2000  
 DEFINITION Sheared DNA-85E2.TF Sheared DNA Trypanosoma brucei genomic clone  
 A2216899 Sheared DNA-85E2, genomic survey sequence.  
 ACCESSION A2216899.1 GI:8434699  
 VERSION GSS.  
 KEYWORDS Trypanosoma brucei  
 SOURCE Trypanosoma brucei  
 ORGANISM Trypanosoma brucei  
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.  
 1 (bases 1 to 558)  
 El-Sayed, N., Zhao, S., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C.,  
 Gerrard, C., Leech, V., de Jong, P., Ulliu, E., Weiville, S., Doneison, J.,  
 Fraser, C. and Adams, M.  
 Determination of clone end sequences from Trypanosoma brucei GUTat  
 10.1 sheared DNA library  
 Unpublished  
 Other\_GSS: Sheared DNA-85E2.TF  
 Contact: Najib M. El-Sayed  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: nelsayed@tigr.org  
 Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared  
 DNA library constructed at TIGR. Clones will be available for  
 distribution through Research Genetics, Alabama, USA. Sheared DNA  
 end sequences search page: <http://www.tigr.org/cdb/mdb/tbdb/>.  
 Seq primer: M13-Forward  
 Class: Shotgun.  
 FEATURES  
 source location/Qualifiers  
 1..558  
 /organism="Trypanosoma brucei"  
 /mol\_type="genomic DNA"  
 /strain="TREU927/4 GUTat 10.1"  
 /db\_xref="taxon:5691"  
 /clone="Sheared DNA-85E2"  
 /clone\_1fb="Sheared DNA"  
 /note="Vector: pUC18; Site 1: SmaI; Constructed at The  
 Institute for Genomic Research (TIGR), Rockville, MD.  
 Genomic DNA isolated from a cloned population of  
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically  
 sheared to give a tight size distribution (approx 2 kb).  
 The v + i method used for the library construction is  
 described in detail in Smith, H.O. and Venter, J.C.  
 (Making small insert libraries for whole genome shotgun  
 sequencing projects. In Genome Sequencing: A Practical  
 Approach, eds. M. Vaudin and B. Barrell, Oxford University  
 Press, 1999)."

BASE COUNT 117 a 192 c 106 g 143 t  
 ORIGIN

Query Match 66.7%; Score 14; DB 28; Length 558;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTGAACGTTTCG 14  
 |||||  
 Db 209 TCGTGAACGTTTCG 222

RESULT 45  
 BM632387 561 bp mRNA linear EST 26-FEB-2002  
 LOCUS BM632387  
 DEFINITION 170006870504190 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
 19600449668153 5', mRNA sequence.  
 ACCESSION BM632387  
 VERSION BM632387.1 GI:18931898  
 KEYWORDS EST.  
 SOURCE Anopheles gambiae (African malaria mosquito)  
 ORGANISM Anopheles gambiae  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
 Anopheles.  
 1 (bases 1 to 561)  
 Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab  
 R., Collins, F.H., Venter, J.C. and Hoffman, S.L.  
 Celera Genomics  
 Contact: Holt R.A.  
 45 W. Gude Dr., Rockville, MD 20850, USA  
 Tel: 240453151  
 Fax: 2404534580  
 Email: Holt@celera.com  
 Plate: NU01004AB row: J column: 23  
 Seq primer: M13 Reverse.  
 FEATURES  
 source location/Qualifiers  
 1..561  
 /organism="Anopheles gambiae"  
 /mol\_type="mRNA"  
 /strain="RSP-ST (Reduced susc. to Permethrin - std.  
 chromosome)"  
 /db\_xref="taxon:7165"  
 /clone="19600449668153"  
 /dev\_stage="Adult"  
 /lab\_host="DHI0b"  
 /clone\_1fb="A.Gam.ad.cDNA1"  
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; whole  
 adult mosquitoes (mixed sex) frozen on liquid nitrogen.  
 cDNA inserts >500 bp cloned directionally into pSport 1.  
 Not I site is 3'. Clones available through the Malaria  
 Research and Reference Reagent Resource Center  
 (www.malaria.mr4.org)."

REFERENCE 1 (bases 1 to 561)  
 Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab  
 R., Collins, F.H., Venter, J.C. and Hoffman, S.L.  
 Celera Genomics  
 Contact: Holt R.A.  
 45 W. Gude Dr., Rockville, MD 20850, USA  
 Tel: 240453151  
 Fax: 2404534580  
 Email: Holt@celera.com  
 Plate: NU01004AB row: J column: 23  
 Seq primer: M13 Reverse.  
 FEATURES  
 source location/Qualifiers  
 1..561  
 /organism="Anopheles gambiae"  
 /mol\_type="mRNA"  
 /strain="RSP-ST (Reduced susc. to Permethrin - std.  
 chromosome)"  
 /db\_xref="taxon:7165"  
 /clone="19600449668153"  
 /dev\_stage="Adult"  
 /lab\_host="DHI0b"  
 /clone\_1fb="A.Gam.ad.cDNA1"  
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; whole  
 adult mosquitoes (mixed sex) frozen on liquid nitrogen.  
 cDNA inserts >500 bp cloned directionally into pSport 1.  
 Not I site is 3'. Clones available through the Malaria  
 Research and Reference Reagent Resource Center  
 (www.malaria.mr4.org)."

BASE COUNT 131 a 148 c 187 g 95 t  
 ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 561;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGAAGCTTCGAGAT 18  
 |||||  
 Db 414 CGAAGCTTCGAGAT 401

RESULT 46  
 BM600003 562 bp mRNA linear EST 25-FEB-2002  
 LOCUS BM600003  
 DEFINITION 17000687050748 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
 19600449725768 5', mRNA sequence.  
 ACCESSION BM600003  
 VERSION BM600003.1 GI:18898107  
 KEYWORDS EST.

SOURCE  
ORGANISM Anopheles gambiae (African malaria mosquito)  
Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
Anopheles.  
REFERENCE 1 (bases 1 to 562)  
AUTHORS Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab  
R., Collins, F.H., Venter, J.C. and Hoffman, S.L.  
TITLE Celera Anopheles gambiae EST project  
JOURNAL Unpublished  
COMMENT Contact: Holt R.A.  
Celera Genomics  
45 W. Gude Dr., Rockville, MD 20850, USA  
Tel: 2404533151  
Fax: 2404534580  
Email: HoltR@celera.com  
Plate: NU01004AYG row: K column: 02  
Seq primer: M13 Reverse.

FEATURES  
source  
1..562  
Location/Qualifiers  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="RSP-ST (Reduced susc. to Permethrin - std.  
chromosome)"  
/db\_xref="taxon:7165"  
/clone="19600449637012"  
/dev\_stage="Adult"  
/lab\_host="DHI0b"  
/clone\_lib="A.Gam.ad.cDNA1"  
/note="Vector: pSport1; Site\_1: SalI; Site\_2: NotI; Whole  
adult mosquitoes (mixed sex) frozen on liquid nitrogen 24  
hours after human blood feeding. cDNA inserts >500 bp  
cloned directionally into pSport 1. Not 1 site is 3'.  
Clones available through the Malaria Research and  
Reference Reagent Resource Center (www.malaria.mr4.org)"

BASE COUNT 132 a 153 c 183 g 94 t

ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 562;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGCTTCGAGAT 18  
|||||  
408 CGAAGCTTCGAGAT 395

Db

RESULT 47  
BM621639 569 bp mRNA linear EST 25-FEB-2002  
LOCUS 17000687447524 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
DEFINITION 19600449637012 5', mRNA sequence.  
ACCESSION BM621639  
VERSION BM621639.1 GI:18920057  
KEYWORDS EST.  
SOURCE Anopheles gambiae (African malaria mosquito)  
ORGANISM Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
Anopheles.  
REFERENCE 1 (bases 1 to 569)  
AUTHORS Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab  
R., Collins, F.H., Venter, J.C. and Hoffman, S.L.  
TITLE Celera Anopheles gambiae EST project  
JOURNAL Unpublished  
COMMENT Contact: Holt R.A.  
Celera Genomics  
45 W. Gude Dr., Rockville, MD 20850, USA  
Tel: 2404533151  
Fax: 2404534580  
Email: HoltR@celera.com  
Plate: NU01004AYL row: I column: 10  
Seq primer: M13 Reverse.

FEATURES  
source  
1..569  
Location/Qualifiers  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="RSP-ST (Reduced susc. to Permethrin - std.  
chromosome)"  
/db\_xref="taxon:7165"  
/clone="19600449637012"  
/dev\_stage="Adult"  
/lab\_host="DHI0b"  
/clone\_lib="A.Gam.ad.cDNA1"  
/note="Vector: pSport1; Site\_1: SalI; Site\_2: NotI; Whole  
adult mosquitoes (mixed sex) frozen on liquid nitrogen.  
cDNA inserts >500 bp cloned directionally into pSport 1.  
Not 1 site is 3'. Clones available through the Malaria  
Research and Reference Reagent Resource Center  
(www.malaria.mr4.org)."

BASE COUNT 135 a 151 c 187 g 96 t

ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 569;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGCTTCGAGAT 18  
|||||  
430 CGAAGCTTCGAGAT 417

Db

RESULT 48  
BM619639 571 bp mRNA linear EST 25-FEB-2002  
LOCUS 17000687440685 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
DEFINITION 19600449657860 5', mRNA sequence.  
ACCESSION BM619639  
VERSION BM619639.1 GI:18918057  
KEYWORDS EST.  
SOURCE Anopheles gambiae (African malaria mosquito)  
ORGANISM Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
Anopheles.  
REFERENCE 1 (bases 1 to 571)  
AUTHORS Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab  
R., Collins, F.H., Venter, J.C. and Hoffman, S.L.  
TITLE Celera Anopheles gambiae EST project  
JOURNAL Unpublished  
COMMENT Contact: Holt R.A.  
Celera Genomics  
45 W. Gude Dr., Rockville, MD 20850, USA  
Tel: 2404533151  
Fax: 2404534580  
Email: HoltR@celera.com  
Plate: NU01004AB6 row: N column: 02  
Seq primer: M13 Reverse.

FEATURES  
source  
1..571  
Location/Qualifiers  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
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chromosome)"  
/db\_xref="taxon:7165"  
/clone="19600449657860"  
/dev\_stage="Adult"  
/lab\_host="DHI0b"  
/clone\_lib="A.Gam.ad.cDNA1"  
/note="Vector: pSport1; Site\_1: SalI; Site\_2: NotI; Whole  
adult mosquitoes (mixed sex) frozen on liquid nitrogen.  
cDNA inserts >500 bp cloned directionally into pSport 1.  
Not 1 site is 3'. Clones available through the Malaria  
Research and Reference Reagent Resource Center  
(www.malaria.mr4.org)."

BASE COUNT 142 a 151 c 188 g 90 t

[illegible]

KEYWORDS EST.  
SOURCE Danio rerio (zebrafish)  
ORGANISM  
REFERENCE  
AUTHORS

TITLE  
JOURNAL  
COMMENT

Danio rerio (zebrafish) unpublished  
Contact: Stephen L. Johnson  
Washington University School of Medicine  
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: zdratish@wustl.edu  
CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:  
Matthew Clark. DNA Sequencing by: Washington University Genome  
Sequencing Center Clone distribution: Genome Systems, St. Louis,  
Missouri (web address: www.genomesystems.com) (email contact:  
info@genomesys.com) and Research Genetics, Huntsville, Alabama  
(web address: www.resgen.com) (email contact: info@resgen.com) and  
Ressourcenzentrum Primatdatenbank, Berlin, Germany (web address:  
www.rzp.de)

Seq primer: T3 RT from Amersham  
High quality sequence stop: 481.

Location/Qualifiers

1. 577  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="IMAGE:3722374"  
/sex="mixed"  
/tissue\_type="26 somite embryos, adult livers, shield  
stage embryos"  
/lab\_host="XLI-blue MRF"  
/clone\_id="Zebrafish Mashu MPIMG ESF"  
/notes="Vector: pSPORT1; Site\_1: NotI; Site\_2: SalI; 1st  
strand cDNA was primed with a Not I - Oligo(dT)15 primer  
[5'-GACCTAGTTCTTAGATCCGACGCCGCCCTTTTTTTTTTTT-3'];  
double-stranded cDNA was ligated to Sal I adaptors (BRL),  
digested with Not I and cloned into the Not I and Sal I  
sites of the pSPORT1 vector (BRL). Library was constructed  
by Matthew Clark (Lehrach lab; ICRP, London and Max Planck  
Institut fuer Molekulare Genetik, Berlin). cDNAs for EST  
analysis were selected following oligonucleotide  
hybridization fingerprinting of arrayed clones from  
zebrafish late somitogenesis (26 ss), adult liver or  
embryonic shield stage (5.5 h) libraries. Fingerprint  
data were used to computationally cluster cDNAs, and a  
single cDNA from each cluster was chosen for sequencing.  
In some cases multiple members of the same cluster were  
sequenced to assess clustering parameters or single clones  
were sequenced additional times to assess quality  
control."

BASE COUNT 140 a 126 c 154 g 157 t  
ORIGIN

Query Match 66.7%; Score 14; DB 9; Length 577;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

7 AACCTCGAGATGA 20  
|||||  
DB 406 AACCTCGAGATGA 419

RESULT 51

BM650798/c 578 bp mRNA linear EST 26-FEB-2002  
 LOCUS 1700068732563 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
 DEFINITION 1960049637545 5', mRNA sequence.  
 ACCESSION BM650798  
 VERSION BM650798.1 GI:18950309  
 KEYWORDS EST.  
 SOURCE Anopheles gambiae (African malaria mosquito)  
 ORGANISM Anopheles gambiae  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
 Anopheles.  
 REFERENCE 1 (bases 1 to 578)  
 AUTHORS Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab  
 TITLE R., Collins,F.H., Venter,J.C. and Hoffman,S.L.  
 JOURNAL Celera Anopheles gambiae EST project  
 COMMENT Unpublished  
 CONTACT: Holt R.A.  
 Celera Genomics  
 45 W. Gude Dr., Rockville, MD 20850, USA  
 Tel: 2404533151  
 Fax: 2404534580  
 Email: HoltRA@celera.com  
 Plate: NU01004AYT row: O column: 15  
 Seq primer: M3 Reverse  
 Location/Qualifiers  
 1..578  
 /organism="Anopheles gambiae"  
 /mol\_type="mRNA"  
 /strain="RSP-ST (Reduced susc. to Permethrin - std.  
 chromosome)"  
 /db\_xref="taxon:7165"  
 /clone="1960049637545"  
 /dev\_stage="Adult"  
 /lab\_host="DH10b"  
 /clone\_lib="A.Gam.ad.cDNA1"  
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole  
 adult mosquitoes (mixed sex) frozen on liquid nitrogen.  
 cDNA inserts >500 bp cloned directionally into pSport 1.  
 Not 1 site is 3'. Clones available through the Malaria  
 Research and Reference Reagent Resource Center  
 (www.malaria.wri.org)."  
 BASE COUNT 138 a 154 c 185 g 101 t  
 ORIGIN  
 Query Match 66.7%; Score 14; DB 12; Length 578;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 5 CGAAGCTTCGAGAT 18  
 |||||  
 |||||  
 Db 426 CGAAGCTTCGAGAT 413  
 RESULT 52 583 bp mRNA linear EST 20-DEC-2001  
 BM279238  
 LOCUS Nb ad1 04E02 M13 Nipoststrongylus brasiliensis uni-zap adult library  
 DEFINITION Nipoststrongylus brasiliensis cDNA clone Nb ad1 04E02 5' similar to  
 ref|NP\_492164.1| (NM\_059763) PZ2 domain (Also known as DHR or GUGP  
 ). (Caenorhabditis, mRNA sequence.  
 ACCESSION BM279238  
 VERSION BM279238.1 GI:17972496  
 KEYWORDS EST.  
 SOURCE Nipoststrongylus brasiliensis  
 ORGANISM Nipoststrongylus brasiliensis  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;  
 Trichostrongyloidea; Heligmonellidae; Nipoststrongylinae;  
 Nipoststrongylus.  
 REFERENCE 1 (bases 1 to 582)  
 AUTHORS Harcus,Y. and Maizels,R.M.  
 TITLE Sequence survey of Nipoststrongylus brasiliensis  
 JOURNAL Unpublished

COMMENT Contact: Maizels RM  
 Institute of Cell, Animal and Population Biology  
 University of Edinburgh  
 Ashworth Labs, West Mains Road, Edinburgh EH93JT, Scotland  
 Tel: +44 131 650 5511  
 Fax: +44 131 650 5450  
 Email: r.maizels@ed.ac.uk  
 The library was prepared by Murray Selkirk, Imperial College,  
 London. Sequencing was performed by Yvonne Harcus, Edinburgh  
 University, UK  
 PCR Primers  
 FORWARD: T3  
 BACKWARD: T7PL  
 Plate: 04 row: B column: 02  
 Seq primer: M13  
 High quality sequence stop: 582.  
 Location/Qualifiers  
 1..582  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:27835"  
 /clone="Nb ad1 04E02"  
 /dev\_stage="adult"  
 /clone\_lib="Nipoststrongylus brasiliensis uni-zap adult  
 library"  
 /note="Vector: pBluescript SK+; The library was prepared  
 in Murray Selkirk's lab, Imperial College, London."  
 BASE COUNT 159 a 135 c 143 g 145 t  
 ORIGIN  
 Query Match 66.7%; Score 14; DB 12; Length 582;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 8 ACGTTCGAGATGAT 21  
 |||||  
 |||||  
 Db 212 ACGTTCGAGATGAT 225  
 RESULT 53 583 bp mRNA linear EST 23-FEB-2001  
 BF157792  
 LOCUS Dn14g06.y1 Sugano Kawakami zebrafish DNA Danio rerio cDNA clone  
 DEFINITION IMAGE:3816778 5', mRNA sequence.  
 ACCESSION BF157792  
 VERSION BF157792.1 GI:11052991  
 KEYWORDS EST.  
 SOURCE Danio rerio (zebrafish)  
 ORGANISM Danio rerio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes  
 ; Cyprinidae; Danio.  
 REFERENCE 1 (bases 1 to 583)  
 AUTHORS Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Rddy  
 S., Hillier,L., Kucaba,T., Martin,T., Beck,C., Wylie,T., Underwood  
 K., Stepcie,W., Theising,B., Allen,M., Bowers,Y., Pearson,B.,  
 Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurr,R., Ritter,E.,  
 Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.  
 and Wilson,R.  
 TITLE Wabnu zebrafish EST Project 1998  
 JOURNAL Unpublished  
 COMMENT Contact: Stephen L. Johnson  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: zbrafish@wustl.edu  
 Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA  
 Sequencing by: Washington University Genome Sequencing Center Clone  
 distribution information can be found through the I.M.A.G.E.  
 Consortium/LNL, send email to: info@image.llnl.gov  
 Seq primer: T3 RT from Amersham  
 High quality sequence stop: 514.

FEATURES  
source  
Location/Qualifiers  
1..583  
/organism="Pantio rerio"  
/mol\_type="mRNA"  
/strain="AB"  
/db\_xref="taxon:7955"  
/clone="IMAGE:3816778"  
/sex="mixed (one male and one female, including unfertilized eggs)"  
/dev\_stage="adult"  
/lab\_host="DH10b (phage resistant)"  
/clone\_lib="Sugano Kawakami zebrafish DR1"  
/note="Vector: pME18s-FL3; Site 1: DraIII (CACTGTCG); Site 2: DraIII (CACCATGTC); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [GTGGCCCTGTCG], digested and cloned into distinct DraIII sites of the pME18s-FL3 vector (5' site CACTGTCG, 3' site CACCATGTC). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science) and kindly donated by Dr. Koichi Kawakami. Custom primers for sequencing: 5' end primer CTCTGCTCTAAAGCTGCG and 3' end primer CGACCTCGACGCTCGACACA."

BASE COUNT  
139 a 148 c 152 g 143 t 1 others

ORIGIN

Query Match 66.7%; Score 14; DB 10; Length 583;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AACGTTTCGAGATCA 20  
|||||  
261 AACGTTTCGAGATCA 274

Db

RESULT 54  
BM630963/c 588 bp mRNA linear EST 26-FEB-2002  
DEFINITION 17000687502159 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
19600449617012 5', mRNA sequence.  
ACCESSION BM630963  
VERSION  
KEYWORDS  
SOURCE EST  
ORGANISM Anopheles gambiae (African malaria mosquito)  
Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anophelinae.  
1 (bases 1 to 588)  
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab R., Collins,F.H., Venter,J.C. and Hoffman,S.L.  
Celera Anopheles gambiae EST project  
Unpublished  
Contact: Holt R.A.  
Celera Genomics  
45 W. Gude Dr., Rockville, MD 20850, USA  
Tel: 2404533151  
Fax: 2404534580  
Email: HoltRA@celera.com  
Plate: NU0100496A row: H column: 02  
Seq primer: M13 Reverse  
Location/Qualifiers  
1..588  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"  
/db\_xref="taxon:7165"  
/clone="19600449617012"  
/dev\_stage="Adult"  
/lab\_host="DH10b"

FEATURES  
source  
Location/Qualifiers  
1..588  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"  
/db\_xref="taxon:7165"  
/clone="19600449617012"  
/dev\_stage="Adult"  
/lab\_host="DH10b"

/clone\_lib="A.Gam.ad.cDNA1"  
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSPORT 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."

BASE COUNT  
143 a 160 c 191 g 94 t

ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 588;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGTTTCGAGAT 18  
|||||  
109 CGAAGTTTCGAGAT 96

Db

RESULT 55  
BM649878/c 592 bp mRNA linear EST 26-FEB-2002  
DEFINITION 17000687369980 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
19600449651232 5', mRNA sequence.  
ACCESSION BM649878  
VERSION  
KEYWORDS  
SOURCE EST  
ORGANISM Anopheles gambiae (African malaria mosquito)  
Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anophelinae.  
1 (bases 1 to 592)  
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab R., Collins,F.H., Venter,J.C. and Hoffman,S.L.  
Celera Anopheles gambiae EST project  
Unpublished  
Contact: Holt R.A.  
Celera Genomics  
45 W. Gude Dr., Rockville, MD 20850, USA  
Tel: 2404533151  
Fax: 2404534580  
Email: HoltRA@celera.com  
Plate: NU0100496C row: I column: 22  
Seq primer: M13 Reverse  
Location/Qualifiers  
1..592  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"  
/db\_xref="taxon:7165"  
/clone="19600449651232"  
/dev\_stage="Adult"  
/lab\_host="DH10b"  
/clone\_lib="A.Gam.ad.cDNA1"  
/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSPORT 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."

BASE COUNT  
138 a 158 c 199 g 97 t

ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 592;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGTTTCGAGAT 18  
|||||  
Db 442 CGAAGTTTCGAGAT 429

RESULT 56  
BM624679/c  
LOCUS  
DEFINITION 17000687491666 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
19600449643241 5', mRNA sequence.  
ACCESSION  
BM624679  
VERSION  
BM624679.1 GI:18924190  
KEYWORDS  
EST.  
SOURCE  
Anopheles gambiae (African malaria mosquito)  
ORGANISM  
Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
Anopheles.  
REFERENCE  
1 (bases 1 to 593)  
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab  
R., Collins, F.H., Venter, J.C. and Hoffman, S.L.  
Celera Anopheles gambiae EST project  
JOURNAL  
Unpublished  
CONTACT: Holt R.A.  
Celera Genomics  
45 W. Gude Dr., Rockville, MD 20850, USA  
Tel: 2404533151  
Fax: 2404534580  
Email: HoltR@celera.com  
Plate: NU01004AY9 row: L column: 23  
Seq primer: M13 Reverse.  
FEATURES  
source  
1..593  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="RSP-ST (Reduced susc. to Permethrin - std.  
chromosome)"  
/db\_xref="taxon:7165"  
/clone="19600449643241"  
/dev\_stage="Adult"  
/lab\_host="DH10B"  
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole  
adult mosquitoes (mixed sex) frozen on liquid nitrogen.  
cDNA inserts >500 bp cloned directionally into pSport 1.  
Not 1 site is 3'. Clones available through the Malaria  
Research and Reference Reagent Resource Center  
(www.malaria.mr4.org)."  
BASE COUNT  
140 a 155 c 184 g 114 t  
ORIGIN  
Query Match 66.7%; Score 14; DB 12; Length 593;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 CGAAGCTTCGAGAT 18  
|||||  
Db 459 CGAAGCTTCGAGAT 446  
RESULT 57  
BM622534/c  
LOCUS  
DEFINITION 17000687476438 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
19600449643086 5', mRNA sequence.  
ACCESSION  
BM622534  
VERSION  
BM622534.1 GI:18922045  
KEYWORDS  
EST.  
SOURCE  
Anopheles gambiae (African malaria mosquito)  
ORGANISM  
Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
Anopheles.  
REFERENCE  
1 (bases 1 to 593)  
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab  
R., Collins, F.H., Venter, J.C. and Hoffman, S.L.  
Celera Anopheles gambiae EST project  
JOURNAL  
Unpublished  
CONTACT: Holt R.A.  
Celera Genomics  
45 W. Gude Dr., Rockville, MD 20850, USA  
Tel: 2404533151  
Fax: 2404534580  
Email: HoltR@celera.com  
Plate: NU01004NBW row: E column: 16  
Seq primer: M13 Reverse.  
FEATURES  
source  
1..593  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
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chromosome)"  
/db\_xref="taxon:7165"  
/clone="19600449625402"  
/dev\_stage="Adult"

JOURNAL  
Unpublished  
CONTACT: Holt R.A.  
Celera Genomics  
45 W. Gude Dr., Rockville, MD 20850, USA  
Tel: 2404533151  
Fax: 2404534580  
Email: HoltR@celera.com  
Plate: NU01004AY9 row: F column: 12  
Seq primer: M13 Reverse.  
FEATURES  
source  
1..593  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="RSP-ST (Reduced susc. to Permethrin - std.  
chromosome)"  
/db\_xref="taxon:7165"  
/clone="19600449643086"  
/dev\_stage="Adult"  
/lab\_host="DH10B"  
/clone\_11b="A.Gam.ad.cDNA1"  
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole  
adult mosquitoes (mixed sex) frozen on liquid nitrogen.  
cDNA inserts >500 bp cloned directionally into pSport 1.  
Not 1 site is 3'. Clones available through the Malaria  
Research and Reference Reagent Resource Center  
(www.malaria.mr4.org)."  
BASE COUNT  
142 a 156 c 194 g 103 t  
ORIGIN  
Query Match 66.7%; Score 14; DB 12; Length 593;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 CGAAGCTTCGAGAT 18  
|||||  
Db 426 CGAAGCTTCGAGAT 413  
RESULT 58  
BM632552/c  
LOCUS  
DEFINITION 17000687504447 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
19600449625402 5', mRNA sequence.  
ACCESSION  
BM632552  
VERSION  
BM632552.1 GI:18932063  
KEYWORDS  
EST.  
SOURCE  
Anopheles gambiae (African malaria mosquito)  
ORGANISM  
Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
Anopheles.  
REFERENCE  
1 (bases 1 to 593)  
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab  
R., Collins, F.H., Venter, J.C. and Hoffman, S.L.  
Celera Anopheles gambiae EST project  
JOURNAL  
Unpublished  
CONTACT: Holt R.A.  
Celera Genomics  
45 W. Gude Dr., Rockville, MD 20850, USA  
Tel: 2404533151  
Fax: 2404534580  
Email: HoltR@celera.com  
Plate: NU01004NBW row: E column: 16  
Seq primer: M13 Reverse.  
FEATURES  
source  
1..593  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="RSP-ST (Reduced susc. to Permethrin - std.  
chromosome)"  
/db\_xref="taxon:7165"  
/clone="19600449625402"  
/dev\_stage="Adult"

```

/1ab_host="DH10b"
/clone_1ib="A.Gam.ad.CDNA1"
/notes="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
(www.malaria.mrt4.org)."
BASE COUNT      148 a      158 c      197 g      92 t
ORIGIN
Query Match      66.7%; Score 14; DB 12; Length 595;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CGAACGTTGAGAT 18
|||||
Db      376 CGAACGTTGAGAT 363

RESULT 59
BM639133      600 bp      mRNA      linear      EST 26-FEB-2002
LOCUS      17000687567918 A.Gam.ad.CDNA1 Anopheles gambiae cDNA clone
DEFINITION      1960044966203 5', mRNA sequence.
ACCESSION      BM639133
VERSION      BM639133.1 GI:18938644
KEYWORDS      EST
SOURCE      Anopheles gambiae (African malaria mosquito)
ORGANISM      Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoides;
Anopheles.
1 (bases 1 to 600)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab
,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
Unpublished
Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltR@celera.com
Plate: NU0100418A row: 1 column: 17
Seq primer: M13 Reverse.
Location/Qualifiers
FEATURES
source
1..600
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
chromosome)"
/db_xref="taxon:7165"
/clone="1960044966203"
/dev_stage="Adult"
/lab_host="DH10b"
/clone_1ib="A.Gam.ad.CDNA1"
/notes="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
(www.malaria.mrt4.org)."
BASE COUNT      144 a      158 c      194 g      104 t
ORIGIN
Query Match      66.7%; Score 14; DB 12; Length 600;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CGAACGTTGAGAT 18
|||||
Db      431 CGAACGTTGAGAT 418

```

```

RESULT 60
A0837727      601 bp      DNA      linear      GSS 30-AUG-1999
LOCUS      HS_5413_B2_D06_77A RPCI-11 Human Male BAC library Homo sapiens
DEFINITION      genomic clone Plate=989 Col=12 Row=H, genomic survey sequence.
ACCESSION      A0837727
VERSION      A0837727.1 GI:5807601
KEYWORDS      GSS.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 601)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,W.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
JOURNAL
MEDLINE
PUBMED
10449764
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Peter de Jong
(plet@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end web Server:
http://www.hsc.washington.edu
Plate: 989 row: H column: 12
Seq primer: T7
Classes: BAC ends
High quality sequence stop: 601.
Location/Qualifiers
FEATURES
source
1..601
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=989 Col=12 Row=H"
/sex="male"
/clone_1ib="RPCI-11 Human Male BAC library"
/notes="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
BASE COUNT      166 a      114 c      116 g      195 t
ORIGIN
Query Match      66.7%; Score 14; DB 28; Length 601;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCGTGCAGCGTTG 14
|||||
Db      552 TCGTGCAGCGTTG 565

RESULT 61
BM621612/c      606 bp      mRNA      linear      EST 25-FEB-2002
LOCUS      17000687447485 A.Gam.ad.CDNA1 Anopheles gambiae cDNA clone
DEFINITION      19600449636865 5', mRNA sequence.
ACCESSION      BM621612
VERSION      BM621612.1 GI:18920030
KEYWORDS      EST.

```

SOURCE  
ORGANISM Anopheles gambiae (African malaria mosquito)  
Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
Anopheles  
1 (bases 1 to 606)  
Holt,R.A., Lin,U.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab  
R., Collins,F.H., Venter,J.C. and Hoffman,S.L.  
Celera Anopheles gambiae EST project  
Unpublished  
COMMENT Contact: Holt R.A.  
Celera Genomics  
45 W. Gude Dr., Rockville, MD 20850, USA  
Tel: 2404533151  
Fax: 2404534580  
Email: HoltR@celera.com  
Plate: NU01004AYL row: C column: 07  
Seq primer: M13 Reverse  
Location/Qualifiers  
1..606  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="RSP-ST (Reduced susc. to Permethrin - std.  
chromosome)"  
/db\_xref="taxon:7165"  
/clone="19600449636865"  
/dev\_stage="Adult"  
/lab\_host="DH10b"  
/clone\_lib="A.Gam.ad.cDNA1"  
/note="Vector: pSPori; Site\_1: SalI; Site\_2: NotI; Whole  
adult mosquitoes (mixed sex) frozen on liquid nitrogen.  
cDNA inserts >500 bp cloned directionally into pSPori 1.  
Not 1 site is 3'. Clones available through the Malaria  
Research and Reference Reagent Resource Center  
(www.malaria.mrc.org)."  
BASE COUNT 155 a 162 c 201 g 88 t  
ORIGIN  
Query Match 66.7%; Score 14; DB 12; Length 606;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 CGAAGCTTCGAGAT 18  
|||||  
Db 336 CGAAGCTTCGAGAT 323  
RESULT 62  
BH416973 606 bp DNA linear GSS 12-DEC-2001  
LOCUS BH416973/C  
DEFINITION 1007052A03.xl 1007 - Rescuedu Grid H Zea mays genomic, genomic  
survey sequence.  
ACCESSION BH416973  
VERSION BH416973.1 GI:17600729  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
Clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 606)  
Walbot,V.  
Maize genomic sequences found using engineered Rescuedu transposon  
Unpublished  
COMMENT Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 1007052 column: 30  
Classes: transposon-tagged.

FEATURES  
source Location/Qualifiers  
1..606  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="mixed background W23/A18/B73"  
/db\_xref="taxon:4577"  
/tissue\_type="leaf"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="1007 - Rescuedu Grid H"  
/note="Organ: leaf; Vector: Rescuedu (engineered from  
pBluescript backbone); Site\_1: BamHI; Site\_2: BglII;  
Rescuedu is a 4.9 Kb, modified maize Mu transposon  
designed to allow plasmid rescue from total genomic DNA.  
Mu elements insert preferentially into transcription  
units. For more information on Rescuedu, go to the  
site 'www.zmmb.iastate.edu' and follow the links for  
'Rescuedu'. Grid H was grown at Berkeley in 2001. DNA  
was extracted from leaf punches, double digested using  
BamHI and BglII, and ligated to form circular plasmids.  
DH10B cells were transformed and then screened on LB  
plates with ampicillin."  
BASE COUNT 143 a 141 c 146 g 174 t 2 others  
ORIGIN  
Query Match 66.7%; Score 14; DB 28; Length 606;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 CGAAGCTTCGAGAT 18  
|||||  
Db 434 CGAAGCTTCGAGAT 421  
RESULT 63  
BM634523 614 bp mRNA linear EST 26-FEB-2002  
LOCUS BM634523/C  
DEFINITION 17000687509206 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
19600449654085 5', mRNA sequence.  
ACCESSION BM634523  
VERSION BM634523.1 GI:18934034  
KEYWORDS EST.  
SOURCE Anopheles gambiae (African malaria mosquito)  
ORGANISM Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
Anopheles  
1 (bases 1 to 614)  
Holt,R.A., Lin,U.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab  
R., Collins,F.H., Venter,J.C. and Hoffman,S.L.  
Celera Anopheles gambiae EST project  
Unpublished  
COMMENT Contact: Holt R.A.  
Celera Genomics  
45 W. Gude Dr., Rockville, MD 20850, USA  
Tel: 2404533151  
Fax: 2404534580  
Email: HoltR@celera.com  
Plate: NU01004AYN row: P column: 19  
Seq primer: M13 Reverse.  
Location/Qualifiers  
1..614  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="RSP-ST (Reduced susc. to Permethrin - std.  
chromosome)"  
/db\_xref="taxon:7165"  
/clone="19600449654085"  
/dev\_stage="Adult"  
/lab\_host="DH10b"  
/clone\_lib="A.Gam.ad.cDNA1"  
/note="Vector: pSPori; Site\_1: SalI; Site\_2: NotI; Whole  
adult mosquitoes (mixed sex) frozen on liquid nitrogen.



CDNA inserts >500 bp cloned directionally into pSport 1.  
Not 1 site is 3'. Clones available through the Malaria  
Research and Reference Reagent Resource Center  
(www.malaria.mr4.org)."

BASE COUNT 153 a 164 c 202 g 95 t

Query Match 66.7%; Score 14; DB 12; Length 614;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACGTCGAGAT 18  
|||||  
364 CGACGTCGAGAT 351

RESULT 64 BM625508 616 bp mRNA linear EST 26-FEB-2002  
LOCUS BM625508/c 17000667493212 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
DEFINITION 19600449662124 5', mRNA sequence.

ACCESSION BM625508.1 GI:18925019  
VERSION BM625508  
KEYWORDS EST.  
SOURCE Anopheles gambiae (African malaria mosquito)  
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
Anopheles.

REFERENCE 1 (bases 1 to 616)  
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab  
R., Collins, F.H., Venter, J.C. and Hoffman, S.L.  
Celera Anopheles gambiae EST project  
Unpublished

TITLE Celera Anopheles gambiae EST project  
JOURNAL Unpublished  
COMMENT Contact: Holt R.A.  
Celera Genomics  
45 W. Gude Dr., Rockville, MD 20850, USA  
Tel: 2404531151  
Fax: 2404534580  
Email: HoltR@celera.com  
Plate: NU0100418B row: O column: 18  
Seq primer: M13 Reverse.

FEATURES  
source 1..616  
Location/Qualifiers  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="RSP-ST (Reduced susc. to Permethrin - std.  
chromosome)"  
/db\_xref="taxon:7165"  
/clone="19600449662124"  
/dev\_stage="Adult"  
/lab\_host="DHI0B"  
/clone\_1lb="A.Gam.ad.cDNA1"  
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole  
adult mosquitoes (mixed sex) frozen on liquid nitrogen.  
cDNA inserts >500 bp cloned directionally into pSport 1.  
Not 1 site is 3'. Clones available through the Malaria  
Research and Reference Reagent Resource Center  
(www.malaria.mr4.org)."

BASE COUNT 156 a 163 c 196 g 101 t

Query Match 66.7%; Score 14; DB 12; Length 616;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACGTCGAGAT 18  
|||||  
34 CGACGTCGAGAT 21

RESULT 65  
AQ880074/c

LOCUS AQ880074 617 bp DNA linear GSS 09-NOV-1999  
DEFINITION HS 4867\_A1 E01 T7A CIT Approved Human Genomic Sperm Library D Homo  
sapiens genomic clone Plate=4867 Col=1 Row=1, genomic survey  
sequence.

ACCESSION AQ880074 GI:6111541

VERSION AQ880074  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 617)  
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.  
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,  
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and  
Hood, L.  
Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

JOURNAL 99380589  
MEDLINE 10449764  
PUBMED  
Contract: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones may be purchased from Research Genetics (info@resgen.com).  
BAC end Web Server: http://www.htsc.washington.edu  
Plate: 4867 row: I column: 1  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 617.

FEATURES  
source 1..617  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="Plate=4867 Col=1 Row=I"  
/sex="male"  
/clone\_1lb="CIT Approved Human Genomic Sperm Library D"  
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in  
E-Coli DH10B"

BASE COUNT 174 a 165 c 118 g 153 t 7 others

Query Match 66.7%; Score 14; DB 28; Length 617;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ACCTTCGAGATCAT 21  
|||||  
510 ACCTTCGAGATCAT 497

RESULT 66 BM591817 619 bp mRNA linear EST 25-FEB-2002  
LOCUS BM591817/c 17000687435900 A.Gam.ad.cDNA.D1001 Anopheles gambiae cDNA clone  
DEFINITION 1960044970335 5', mRNA sequence.

ACCESSION BM591817  
VERSION BM591817  
KEYWORDS EST.  
SOURCE Anopheles gambiae (African malaria mosquito)  
ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
Anopheles.

REFERENCE 1 (bases 1 to 619)  
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab  
R., Collins, F.H., Venter, J.C. and Hoffman, S.L.  
Celera Anopheles gambiae EST project  
Unpublished

TITLE Celera Anopheles gambiae EST project  
JOURNAL Unpublished

## COMMENT

Contact: Holt R.A.  
Celera Genomics  
45 W. Gude Dr., Rockville, MD 20850, USA  
Tel.: 240453151  
Fax: 2404534580  
Email: HoltR@celera.com  
Plate: NU01009UV row: 1 column: 09  
Seq primer: M13 Reverse.  
Location/Qualifiers

## FEATURES

## source

1..619

/organism="Anopheles gambiae"

/mol\_type="mRNA"

/strain="RSP-ST (reduced suc. to Permethrin - std.

chromosome)"

/db\_xref="taxon:7165"

/dev\_stage="Adult"

/lab\_host="DH10b"

/clone\_lib="A.Gam.ad.cDNA.blood1"

/note="Vector: pSport1; Site\_1: SalI; Site\_2: NotI; Whole  
adult mosquitoes (mixed sex) frozen on liquid nitrogen 24  
hours after human blood feeding. cDNA inserts >500 bp  
cloned directionally into pSport 1. Not 1 site is 3'.

Clones available through the Malaria Research and  
Reference Reagent Resource Center (www.malaria.mr4.org)"

## BASE COUNT

146 a 160 c 199 g 114 t

## ORIGIN

## Query Match

Best Local Similarity 66.7%; Score 14; DB 12; Length 619;  
100.0%; Pred. No. 3.2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTCGACGCTTCG 14

Db 257 TCGTCGACGCTTCG 244

## RESULT

## LOCUS

CC120030/c

## DEFINITION

CC120030 627 bp DNA linear GSS 16-APR-2003  
NDL.76020.T7 Notre Dame Liverpool Aedes aegypti genomic clone  
NDL.76020, genomic survey sequence.

## ACCESSION

CC120030.1 GI:29989085

## VERSION

GSS.

## KEYWORDS

Aedes aegypti

## SOURCE

Aedes aegypti

## ORGANISM

Aedes aegypti

## REFERENCE

Aedes aegypti

## AUTHORS

Aedes aegypti

## TITLE

Aedes aegypti

## JOURNAL

Aedes aegypti

## COMMENT

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.  
1 (bases 1 to 627)  
Loftus, B., Shetty, J., Knudson, D. and Severson, D.  
BAC end sequencing of Aedes aegypti  
Unpublished  
Other GSSs: NDL.76020.SP6  
Contact: Brendan Loftus  
Department of Eukaryotic Genomics  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-3543  
Fax: 301-838-0208  
Email: ente@tigr.org  
Library was provided by David Severson  
Seq primer: T7  
Classes: BAC ends.

## FEATURES

## source

1..627

/organism="Aedes aegypti"

/mol\_type="genomic DNA"

/strain="Liverpool"

/db\_xref="taxon:7159"

/clone\_lib="NDL.76020"

/clone\_lib="Notre Dame Liverpool"

/note="Vector: pECBAC1; Site\_1: Hind III; The library was

prepared from whole body tissue of newly hatched L1 larvae  
by David Severson at the University of Notre Dame and  
Hongbin Zhang"

## BASE COUNT

159 a 148 c 149 g 171 t

## ORIGIN

## Query Match

Best Local Similarity 66.7%; Score 14; DB 29; Length 627;  
100.0%; Pred. No. 3.2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTCGACGCTTCG 14

Db 587 TCGTCGACGCTTCG 574

## RESULT

68

## LOCUS

AW288450/c

## DEFINITION

AW288450

## ACCESSION

AW288450

## VERSION

AW288450.1

## KEYWORDS

EST.

## SOURCE

Trichuris muris

## ORGANISM

Trichuris muris

## REFERENCE

Trichuris muris

## AUTHORS

Trichuris muris

## TITLE

Trichuris muris

## COMMENT

Trichuris muris

## JOURNAL

Trichuris muris

## UNPUBLISHED

Trichuris muris

## CONTACT

Trichuris muris

## INSTITUTE

Trichuris muris

## UNIVERSITY

Trichuris muris

## ADDRESS

Trichuris muris

## CITY

Trichuris muris

## COUNTRY

Trichuris muris

## PUBLISHED

Trichuris muris

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Trichuris muris

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Trichuris muris

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Trichuris muris

## PUBLISHED

Trichuris muris

## PUBLISHED

Trichuris muris

## PUBLISHED

Trichuris muris

Db 363 AACGTTGAGATGA 350

RESULT 69  
LOCUS BM641079 628 bp mRNA linear EST 26-FEB-2002  
DEFINITION 17000687307001 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
1960044965480 5', mRNA sequence.  
BM641079  
ACCESSION BM641079  
VERSION BM641079.1 GI:18940590  
KEYWORDS EST.  
SOURCE Anopheles gambiae (African malaria mosquito)  
ORGANISM Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.  
1 (bases 1 to 628)  
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab  
,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.  
Celera Anopheles gambiae EST project  
Unpublished  
COMMENT Contact: Holt R.A.  
Celera Genomics  
45 W. Gude Dr., Rockville, MD 20850, USA  
Tel: 2404533151  
Fax: 2404534580  
Email: HoltRA@celera.com  
Plate: NU010049WT row: N column: 04  
Seq primer: M13 Reverse.  
Location/Qualifiers  
1..628  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="RSP-ST (Reduced susc. to Permethrin - std.  
chromosome)"  
/db\_xref="taxon:7165"  
/clone="19600449621382"  
/dev\_stage="Adult"  
/lab\_host="DH10b"  
/clone\_lib="A.Gam.ad.cDNA1"  
/note="Vector: pSport1; Site\_1: SalI; Site\_2: NotI; Whole  
adult mosquitoes (mixed sex) frozen on liquid nitrogen.  
cDNA inserts >500 bp cloned directionally into pSport 1.  
Not 1 site is 3'. Clones available through the Malaria  
Research and Reference Reagent Resource Center  
(www.malaria.mr4.org)."

BASE COUNT 153 a 163 c 208 g 104 t

ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 628;  
Best Local Similarity 100.0%; Pred.No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGCTTCGAGAT 18  
|||||  
382 CGAAGCTTCGAGAT 369

Db

RESULT 70  
LOCUS BM622163 629 bp mRNA linear EST 26-FEB-2002  
DEFINITION 17000687475928 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
1960044965480 5', mRNA sequence.  
BM622163  
ACCESSION BM622163  
VERSION BM622163.1 GI:18921686  
KEYWORDS EST.  
SOURCE Anopheles gambiae (African malaria mosquito)  
ORGANISM Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.  
1 (bases 1 to 629)  
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab

TITLE  
JOURNAL  
COMMENT  
R., Collins,F.H., Venter,J.C. and Hoffman,S.L.  
Unpublished  
Contact: Holt R.A.  
Celera Genomics  
45 W. Gude Dr., Rockville, MD 20850, USA  
Tel: 2404533151  
Fax: 2404534580  
Email: HoltRA@celera.com  
Plate: NU010049WT row: A column: 06  
Seq primer: M13 Reverse.  
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BASE COUNT 139 a 166 c 201 g 123 t

ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 629;  
Best Local Similarity 100.0%; Pred.No. 3.2e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGCTTCGAGAT 18  
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485 CGAAGCTTCGAGAT 472

Db

RESULT 71  
LOCUS BM655453 629 bp mRNA linear EST 26-FEB-2002  
DEFINITION 17000687386557 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
19600449627614 5', mRNA sequence.  
BM655453  
ACCESSION BM655453  
VERSION BM655453.1 GI:18954964  
KEYWORDS EST.  
SOURCE Anopheles gambiae (African malaria mosquito)  
ORGANISM Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.  
1 (bases 1 to 629)  
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab  
,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.  
Celera Anopheles gambiae EST project  
Unpublished  
COMMENT Contact: Holt R.A.  
Celera Genomics  
45 W. Gude Dr., Rockville, MD 20850, USA  
Tel: 2404533151  
Fax: 2404534580  
Email: HoltRA@celera.com  
Plate: NU010049VY row: A column: 20  
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chromosome)"  
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/clone_lib="A.Gam.ad.cDNA1"
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adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
(www.malaria.mr4.org)."
BASE COUNT      150 a      168 c      216 g      95 t
ORIGIN

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CGACGTTGAGAT 18
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302 CGACGTTGAGAT 289

RESULT 72
BM625565/c      631 bp      mRNA      linear      EST 26-FEB-2002
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ACCESSION      BM625565
VERSION      BM625565.1 GI:18925076
KEYWORDS      EST
SOURCE      Anopheles gambiae (African malaria mosquito)
ORGANISM      Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anophelinae.
1 (bases 1 to 631)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab
R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
Unpublished
Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltRA@celera.com
Plate: NU010049M1 row: L column: 02
Seq primer: M13 Reverse
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1..631
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/dev_stage="Adult"
/lab_host="DHI0b"
/clone_lib="A.Gam.ad.cDNA1"
/notes="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
(www.malaria.mr4.org)."
BASE COUNT      153 a      162 c      209 g      107 t
ORIGIN

Query Match      66.7%; Score 14; DB 12; Length 631;
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CGACGTTGAGAT 18
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302 CGACGTTGAGAT 18

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Db      389 CGACGTTGAGAT 376

RESULT 73
BM654222/c      631 bp      mRNA      linear      EST 26-FEB-2002
LOCUS      17000687380327 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
DEFINITION      19600449631529 5', mRNA sequence.
ACCESSION      BM654222
VERSION      BM654222.1 GI:18953733
KEYWORDS      EST
SOURCE      Anopheles gambiae (African malaria mosquito)
ORGANISM      Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anophelinae.
1 (bases 1 to 631)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab
R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
Unpublished
Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltRA@celera.com
Plate: NU010049M1 row: D column: 23
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adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
(www.malaria.mr4.org)."
BASE COUNT      152 a      162 c      207 g      110 t
ORIGIN

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|||||
407 CGACGTTGAGAT 394

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DEFINITION      1960044978154 5', mRNA sequence.
ACCESSION      BM597192
VERSION      BM597192.1 GI:18895295
KEYWORDS      EST
SOURCE      Anopheles gambiae (African malaria mosquito)
ORGANISM      Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anophelinae.
1 (bases 1 to 633)

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AUTHORS Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab  
 TITLE R., Collins,F.H., Venter,J.C. and Hoffman,S.L.  
 JOURNAL CelerA Anopheles gambiae EST project  
 COMMENT Unpublished  
 Contact: Holt R.A.  
 CelerA Genomics  
 45 W. Gude Dr., Rockville, MD 20850, USA  
 Tel: 2404533151  
 Fax: 2404534580  
 Email: HoltR@celera.com  
 Place: NU010049VS row: M column: 20  
 Seq primer: M13 Reverse.

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 hours after human blood feeding. cDNA inserts >500 bp  
 cloned directionally into pSport 1. Not 1 site is 3'.  
 Clones available through the Malaria Research and  
 Reference Reagent Resource Center (www.malaria.mr4.org)"  
 BASE COUNT 152 a 163 c 208 g 110 t  
 ORIGIN

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 Qy 5 CGAAGCTTCGAGAT 18  
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 Db 407 CGAAGCTTCGAGAT 394

RESULT 75 636 bp mRNA linear EST 26-FEB-2002  
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 DEFINITION 19600448419407 5', mRNA sequence.  
 BM636272  
 ACCESSION BM636272.1 GI:18935783  
 VERSION  
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 SOURCE  
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 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
 Anopheles.  
 1 (bases 1 to 636)  
 Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab  
 R., Collins,F.H., Venter,J.C. and Hoffman,S.L.  
 CelerA Anopheles gambiae EST project  
 Unpublished  
 Contact: Holt R.A.  
 CelerA Genomics  
 45 W. Gude Dr., Rockville, MD 20850, USA  
 Tel: 2404533151  
 Fax: 2404534580  
 Email: HoltR@celera.com  
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 Seq primer: M13 Reverse.

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 adult mosquitoes (mixed sex) frozen on liquid nitrogen.  
 cDNA inserts >500 bp cloned directionally into pSport 1.  
 Not 1 site is 3'. Clones available through the Malaria  
 Research and Reference Reagent Resource Center  
 (www.malaria.mr4.org)."  
 BASE COUNT 158 a 168 c 209 g 101 t  
 ORIGIN

Query Match 66.7% Score 14; DB 12; Length 636;  
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Qy 5 CGAAGCTTCGAGAT 18  
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 Db 369 CGAAGCTTCGAGAT 356

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 Job time : 1320 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 17, 2003, 09:15:23 ; Search time 147 Seconds  
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385.634 Million cell updates/sec

Title: US-10-033-243-132

Perfect score: 21  
Sequence: 1 tcgcgcagcctcgatgatc 21

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 2552756 seqs, 1349719017 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
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Post-processing: Listing first 100 summaries

Database : N\_GeneSeq\_19Jun03.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	19	90.5	19	24	ABO75170 ISS immunomodulato
3	19	90.5	22	24	ABO75181 ISS immunomodulato
4	16	76.2	18	24	ABO75165 ISS immunomodulato
5	15	71.4	20	24	AAV32079 Double-stranded im
6	15	71.4	22	19	AAV32079 Nucleotide sequenc
7	15	71.4	22	20	AAV36624 ISS-ON DY1018 nuc
8	15	71.4	22	20	AAV80105 Oligo used in expe

9	15	71.4	22	20	AAV80096 Immunomodulatory o
10	15	71.4	22	20	AAV80097 Immunomodulatory o
11	15	71.4	22	20	AAV80102 Immunomodulatory o
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15	15	71.4	22	21	AAV80101 CpG adjuvant oligo
16	15	71.4	22	21	AAV80101 Immunostimulatory
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## ALIGNMENTS

RESULT 1  
ABQ75182 standard; DNA; 21 BP.

ABQ75182; (first entry)  
ISS immunomodulatory oligonucleotide SEQ ID NO:132.

Immunomodulatory sequence; ISS: immunomodulatory; immune response;  
allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;  
idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;  
malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;  
immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;  
virucide; antibacterial; protozoacide; ss.

Synthetic.

WO200252002-A2.

04-JUL-2002.

27-DEC-2001; 2001WO-US50821.

27-DEC-2000; 2000US-258675P.

(DYNA-) DYNAVAX TECHNOLOGIES CORP.

Fearon KL, Dina D;

WPI; 2002-657426/70.

Immunomodulatory polynucleotide for modulating an immune response in a  
subject suffering from disorders associated with Th2-type immune  
response, e.g. allergy, or infectious disease, comprises an  
immunostimulatory sequence

Claim 4; Page 21; 95pp; English.

The present invention describes an immunomodulatory polynucleotide (I)  
comprising an immunostimulatory sequence (ISS). Also described: (1) an  
immunomodulatory composition comprising (I); (2) an immunomodulatory  
polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a  
biodegradable MC, where the MC is less than 10 micrometre in size; and  
(3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,  
antibacterial and protozoacide activities, and can be used as a modulator  
of immune response. (I) is useful for modulating an immune response in an  
individual suffering from disorders associated with a Th2-type immune

response, especially an allergy or asthma, or an infectious disease. (I)  
is also useful for increasing interferon-gamma (IFN-gamma) in an  
individual having idiopathic pulmonary fibrosis, or IFN-alpha in an  
individual having a viral infection. (I) is further useful for  
ameliorating a symptom of an infectious disease caused by a cellular  
pathogen such as mycobacterial disease, malaria, leishmaniasis,  
toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a  
symptom of an immunoglobulin E (IgE)-related disorder, preferably an  
allergy-related disorder, in particular asthma in an individual. The  
present sequence represents an immunomodulatory oligonucleotide from  
the present invention.

Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 other;

Query Match 100.0%; Score 21; DB 24; Length 21;

Best Local Similarity 100.0%; Pred. No. 0.0064;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TCGTGAACGTTGAGATGAT 21

1 TCGTGAACGTTGAGATGAT 21

ABQ75170 standard; DNA; 19 BP.

ABQ75170;

05-NOV-2002 (first entry)

ISS immunomodulatory oligonucleotide SEQ ID NO:19.

Immunostimulatory sequence; ISS: immunomodulatory; immune response;  
allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;  
idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;  
malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;  
immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;  
virucide; antibacterial; protozoacide; ss.

Synthetic.

WO200252002-A2.

04-JUL-2002.

27-DEC-2001; 2001WO-US50821.

27-DEC-2000; 2000US-258675P.

(DYNA-) DYNAVAX TECHNOLOGIES CORP.

Fearon KL, Dina D;

WPI; 2002-657426/70.

Immunomodulatory polynucleotide for modulating an immune response in a  
subject suffering from disorders associated with Th2-type immune  
response, e.g. allergy, or infectious disease, comprises an  
immunostimulatory sequence

Claim 4; Page 20; 95pp; English.

The present invention describes an immunomodulatory polynucleotide (I)  
comprising an immunostimulatory sequence (ISS). Also described: (1) an  
immunomodulatory composition comprising (I); (2) an immunomodulatory  
polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a  
biodegradable MC, where the MC is less than 10 micrometre in size; and  
(3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,  
antibacterial and protozoacide activities, and can be used as a modulator  
of immune response. (I) is useful for modulating an immune response in an  
individual suffering from disorders associated with a Th2-type immune  
response, especially an allergy or asthma, or an infectious disease. (I)



CC is also useful for increasing interferon-gamma (IFN-gamma) in an  
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an  
CC individual having a viral infection. (1) is further useful for  
CC ameliorating a symptom of an infectious disease caused by a cellular  
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,  
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a  
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an  
CC allergy-related disorder, in particular asthma in an individual. The  
CC present sequence represents an immunomodulatory oligonucleotide from  
CC the present invention.

XX SQ Sequence 19 BP; 4 A; 4 C; 6 G; 5 T; 0 other;

Query Match 90.5%; Score 19; DB 24; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.092;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTGAACGTTCCGAGATG 19  
|||  
DB 1 TCGTGAACGTTCCGAGATG 19

RESULT 3  
ABQ75181  
ID ABQ75181 standard; DNA; 22 BP.  
XX  
AC ABQ75181;  
XX  
DT 05-NOV-2002 (first entry)  
XX

DE ISS immunomodulatory oligonucleotide SEQ ID NO:30.  
XX  
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;  
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;  
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;  
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;  
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;  
KW virucide; antibacterial; protozoacide; ss.

XX OS Synthetic.  
XX  
XX PN WO200252002-A2.  
XX

XX PD 04-JUL-2002.  
XX

XX PF 27-DEC-2001; 2001WO-US50821.  
XX

XX PR 27-DEC-2000; 2000US-258675P.  
XX

XX PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
XX

XX PI Fearon KL, Dina D;  
XX

XX DR WPI; 2002-657426/70.  
XX

XX PT Immunomodulatory polynucleotide for modulating an immune response in a  
XX PT subject suffering from disorders associated with Th2-type immune  
XX PT response, e.g. allergy, or infectious disease, comprises an  
XX PT immunostimulatory sequence -  
XX  
XX PS

XX Example 1; Page 21; 95pp; English.

XX The present invention describes an immunomodulatory polynucleotide (1)  
XX comprising an immunostimulatory sequence (ISS). Also described: (1) an  
XX immunomodulatory composition comprising (1); (2) an immunomodulatory  
XX polynucleotide/microcarrier (IMP/MC) complex, comprising (1) linked to a  
XX biodegradable MC, where the MC is less than 10 micrometre in size; and  
XX (3) a kit comprising (1). (1) has antiallergic, antiasthmatic, virucide,  
XX antibacterial and protozoacide activities, and can be used as a modulator  
XX of immune response. (1) is useful for modulating an immune response in an  
XX individual suffering from disorders associated with a Th2-type immune  
XX response, especially an allergy or asthma, or an infectious disease. (1)  
XX is also useful for increasing interferon-gamma (IFN-gamma) in an

CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an  
CC individual having a viral infection. (1) is further useful for  
CC ameliorating a symptom of an infectious disease caused by a cellular  
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,  
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a  
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an  
CC allergy-related disorder, in particular asthma in an individual. The  
CC present sequence represents an immunomodulatory oligonucleotide from  
CC the present invention.

XX SQ Sequence 22 BP; 5 A; 4 C; 7 G; 6 T; 0 other;

Query Match 90.5%; Score 19; DB 24; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.091;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTGAACGTTCCGAGATG 19  
|||  
DB 4 TCGTGAACGTTCCGAGATG 22

RESULT 4  
ABQ75165  
ID ABQ75165 standard; DNA; 18 BP.  
XX  
AC ABQ75165;  
XX  
DT 05-NOV-2002 (first entry)  
XX

DE ISS immunomodulatory oligonucleotide SEQ ID NO:14.  
XX  
KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;  
KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;  
KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;  
KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;  
KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;  
KW virucide; antibacterial; protozoacide; ss.

XX OS Synthetic.  
XX  
XX PN WO200252002-A2.  
XX

XX PD 04-JUL-2002.  
XX

XX PF 27-DEC-2001; 2001WO-US50821.  
XX

XX PR 27-DEC-2000; 2000US-258675P.  
XX

XX PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
XX

XX PI Fearon KL, Dina D;  
XX

XX DR WPI; 2002-657426/70.  
XX

XX PT Immunomodulatory polynucleotide for modulating an immune response in a  
XX PT subject suffering from disorders associated with Th2-type immune  
XX PT response, e.g. allergy, or infectious disease, comprises an  
XX PT immunostimulatory sequence -  
XX  
XX PS

XX Example 1; Page 20; 95pp; English.

XX The present invention describes an immunomodulatory polynucleotide (1)  
XX comprising an immunostimulatory sequence (ISS). Also described: (1) an  
XX immunomodulatory composition comprising (1); (2) an immunomodulatory  
XX polynucleotide/microcarrier (IMP/MC) complex, comprising (1) linked to a  
XX biodegradable MC, where the MC is less than 10 micrometre in size; and  
XX (3) a kit comprising (1). (1) has antiallergic, antiasthmatic, virucide,  
XX antibacterial and protozoacide activities, and can be used as a modulator  
XX of immune response. (1) is useful for modulating an immune response in an  
XX individual suffering from disorders associated with a Th2-type immune  
XX response, especially an allergy or asthma, or an infectious disease. (1)  
XX is also useful for increasing interferon-gamma (IFN-gamma) in an  
XX individual having idiopathic pulmonary fibrosis, or IFN-alpha in an

CC individual having a viral infection. (1) is further useful for  
 CC ameliorating a symptom of an infectious disease caused by a cellular  
 CC pathogen such as mycobacterial disease, malaria, leishmaniasis,  
 CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a  
 CC symptom of an immunoglobulin E (IgE)-related disorder, preferably, an  
 CC allergy-related disorder, in particular asthma in an individual. The  
 CC present sequence represents an immunomodulatory oligonucleotide from  
 CC the present invention.

CC Sequence 18 BP; 4 A; 4 C; 5 G; 5 T; 0 other;

CC Query Match 76.2%; Score 16; DB 24; Length 18;

CC Best Local Similarity 100.0%; Pred. No. 5;

CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 4 TCGAAGTTGAGATG 19  
 CC Db 3 TCGAAGTTGAGATG 18

CC RESULT 5

CC AAD24905 standard; DNA; 20 BP.

CC AC AAD24905;

CC DT 12-MAR-2002 (first entry)

CC DE Double-stranded immunostimulatory oligodeoxynucleotide (ISS-ODN).

CC Cell death; DNA damage; DNA-dependent protein kinase; DNA-PK; necrosis;  
 CC immune response; apoptosis; Alzheimer's disease; Parkinson's disease;  
 CC rheumatoid arthritis; inflammation; osteoporosis; myocardial infarction;  
 CC liver disease; reperfusion injury; carcinoma; multiple sclerosis; stroke;  
 CC amyotrophic lateral sclerosis; Acquired Immune Deficiency Syndrome; AIDS;  
 CC head injury damage; aplastic anaemia; tumour; organ transplantation;  
 CC cerebral infarction; follicular lymphomas; systemic lupus erythematosus;  
 CC viral infection; glomerulonephritis; apoptosis; autoimmune disorder;  
 CC sepsis; immunostimulatory oligodeoxynucleotide; ISS-ODN; ds.

CC OS Unidentified.

CC PN WO200185910-A2.

CC PD 15-NOV-2001.

CC PF 04-MAY-2001; 2001WO-US14508.

CC PR 05-MAY-2000; 2000US-202274P.

CC PR 17-JAN-2001; 2001US-262321P.

CC PA (REGC ) UNIV CALIFORNIA.

CC PI Raz E, Lois AF, Takabayashi K;

CC DR WPI; 2002-062244/08.

CC Modulating cell death or reducing DNA damage in eukaryotic cells,  
 CC useful for reducing cell death in individual or organ, comprises  
 CC contacting cell with agent modulating biological activity of  
 CC DNA-dependent protein kinase -

CC Example 1; Page 31; 57pp; English.

CC The invention relates to a method for modulating cell death or reducing  
 CC DNA damage in an eukaryotic cell by contacting the cell with an agent  
 CC that modulates the biological activity of DNA-dependent protein kinase  
 CC (DNA-PK). The invention also relates nucleic acids which modulate the  
 CC immune response binding to Ku antigen, resulting in activation of DNA-PK.  
 CC The method is useful for modulating cell death or reducing DNA damage in  
 CC an eukaryotic cell, for treating any disorder resulting from a genotoxic  
 CC insert to a cell e.g., necrosis, apoptosis. The method is also useful  
 CC for treating cell death-related indications such as Alzheimer's disease,

CC Parkinson's disease, rheumatoid arthritis, septic shock, stroke,  
 CC central nervous system inflammation, osteoporosis, degenerative liver  
 CC disease, cerebellar degeneration, reperfusion injury, multiple sclerosis,  
 CC amyotrophic lateral sclerosis, myocardial infarction, head injury damage,  
 CC acquired immunodeficiency syndrome (AIDS), aplastic anaemia, cerebral  
 CC infarction, bypass heart surgery, organ transplantation. The method is  
 CC also useful for treating follicular lymphomas, carcinomas, autolymphoma,  
 CC disorders (systemic lupus erythematosus), hormone dependent tumours,  
 CC immune mediated glomerulonephritis; apoptosis and viral infections. The  
 CC present sequence is immunostimulatory oligodeoxynucleotide (ISS-ODN)  
 CC used for identifying ISS-binding protein, which is used in the  
 CC exemplification of the invention.

CC SQ Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 other;

CC Query Match 71.4%; Score 15; DB 24; Length 20;

CC Best Local Similarity 100.0%; Pred. No. 19; 0; Indels 0; Gaps 0;

CC Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 6 GAACGTTGAGATGA 20  
 CC Db 6 GAACGTTGAGATGA 20

CC RESULT 6

CC AAV32079 standard; DNA; 22 BP.

CC AC AAV32079;

CC DT 09-SEP-1998 (first entry)

CC DE Nucleotide sequence of DY1018.

CC DY1018, beta-gal. ISS-PN/IMW, antigen; immune response; antibody;  
 CC immunisation; anaphylaxis; IgE; retinopathies; ss.

CC OS synthetic.

CC FH Key Location/Qualifiers

CC FT modified\_base 1.22

CC FT /tag= a

CC FT /note= "phosphothioate backbone"

CC PN WO9816247-A1.

CC PD 23-APR-1998.

CC PF 09-OCT-1997; 97WO-US19004.

CC PR 11-OCT-1996; 96US-0028118.

CC PA (REGC ) UNIV CALIFORNIA.

CC PI Carson DA, Raz E, Roman M;

CC DR WPI; 1998-261028/23.

CC New immunomodulatory compositions - comprising an antigen conjugated  
 CC to a polynucleotide that contains an immunostimulatory sequence

CC Example 1; Page 36; 69pp; English.

CC This is the nucleotide sequence of DY1018, which is conjugated to  
 CC beta-gal to form ISS-PN/IMW, comprising an immunomodulatory molecule  
 CC (IMW), which comprises an antigen conjugated to a polynucleotide  
 CC (PN) that contains at least one immunostimulatory nucleotide sequence  
 CC (ISS). The conjugate synergistically boost the magnitude of the host  
 CC immune response against an antigen to a level greater than the host  
 CC immune response to either the IMW, antigen or ISS-PN alone. These  
 CC responses to ISS-PN/IMW conjugates are particularly acute during  
 CC the important early phase of the host immune response to an antigen.  
 CC The ISS-PN/IMW conjugates boost both humoral (antibody) and cellular

(Th1 type) immune responses of the host. Thus, use of the method to boost the immune responsiveness of a host to subsequent challenge by a sensitising antigen without immunisation avoids the risk of Th2-mediated, immunisation-induced anaphylaxis by suppressing IgE production in response to the antigen challenge. The conjugates can also be used to combat pathogenic infection and to stimulate therapeutic angiogenesis to treat conditions in which localised blood flow plays a significant etiological role, e.g. retinopathies.

XX  
CC Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

XX  
SQ

Query Match 71.4%; Score 15; DB 19; Length 22;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 GAACGTCGAGATGA 20  
|||  
8 GAACGTCGAGATGA 22

Db

RESULT 7  
AA36624  
ID AA36624 standard; DNA; 22 BP.  
XX  
AC AA36624;  
XX  
XX 09-JUL-1999 (first entry)  
XX  
XX ISS-ODN DY1018 nucleotide sequence.  
XX  
XX  
XX Antigen-stimulated inflammation; immunostimulatory oligonucleotide;  
XX granulocyte-mediated tissue inflammation; Th2 type immune response;  
XX immune responsiveness modulation; idiopathic hypersensitivity; syndrome;  
XX cutaneous basophil hypersensitivity; ISS-ODN; asthma; nasal polyposis;  
XX allergic rhinitis; atopic dermatitis; allergic conjunctivitis;  
XX eosinophilic fasciitis; therapy; ss.  
XX  
XX Synthetic.  
XX  
XX WO9911275-A2.  
XX  
XX 11-MAR-1999.  
XX  
XX 04-SEP-1998; 98WO-US18382.  
XX  
XX 05-SEP-1997; 97US-0927120.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX  
XX Ray E;  
XX  
XX WPI, 1999-312404/26.  
XX  
XX  
XX Reducing antigen-stimulated granulocyte-mediated inflammation  
XX  
XX Example 2; Page 30; 69pp; English.

XX  
CC This is the ISS-ODN DY1018 nucleotide sequence.  
XX The invention relates to a method for preventing or reducing  
XX antigen-stimulated, granulocyte-mediated tissue inflammation in a mammal,  
XX by administering an immunostimulatory oligonucleotide (ISS-ODN), where:  
XX (a) reduction in, or the absence of, a Th2 type immune response is  
XX measured; or (b) there is a reduction or absence of other clinical signs  
XX of inflammation in the host after antigen challenge. The method is used  
XX to reduce or suppress granulocyte-mediated inflammation in a host tissue,  
XX and to modulate the host's immune responsiveness to an antigen,  
XX particularly where the subject suffers from asthma, nasal polyposis,  
XX allergic rhinitis, atopic dermatitis, allergic conjunctivitis,  
XX eosinophilic fasciitis, idiopathic hypersensitivity syndrome, or  
XX cutaneous basophil hypersensitivity. Unlike prior art treatment by  
XX antigen immunisation, the method is an antigen-independent method,  
XX and avoids host production of both interleukin-4 (IL-4), which carries  
XX risk of anaphylaxis, and IL-5 which actually encourages granulocyte

CC adhesion to endothelia.

XX  
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

XX  
SQ

Query Match 71.4%; Score 15; DB 20; Length 22;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 GAACGTCGAGATGA 20  
|||  
8 GAACGTCGAGATGA 22

Db

RESULT 8  
AAV80105/C  
ID AAV80105 standard; DNA; 22 BP.  
XX  
XX  
XX AAV80105;  
XX  
XX 12-MAR-1999 (first entry)  
XX  
XX  
XX Oligo used in experiments for stimulation of cytokine production.  
XX  
XX  
XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
XX ISS; cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
XX human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
XX B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.  
XX  
XX Synthetic.  
XX  
XX WO985495-A2.  
XX  
XX 10-DEC-1998.  
XX  
XX 05-JUN-1998; 98WO-US11578.  
XX  
XX 06-JUN-1997; 97US-0048793.  
XX  
XX  
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
XX  
XX Dina D. Roman M. Schwartz D;  
XX  
XX WPI, 1999-059898/05.  
XX  
XX  
XX Immunostimulatory oligonucleotides regulate the immune system - and  
XX contain an immune-stimulating octanucleotide sequence; for treating  
XX cancer, allergic and infectious diseases  
XX  
XX Example 1; Page 29; 63pp; English.

XX  
CC The invention relates to immunomodulatory oligonucleotides that comprise  
XX at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
XX sequences are selected from the group consisting of AACGTTCC, AACGTTCC,  
XX GACGTTCC, and GACGTTCC. The immunomodulatory sequences are used to treat  
XX patients needing immune regulation, such as those suffering from cancer,  
XX an allergic disease and asthma. They are also used to prevent infectious  
XX diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
XX and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
XX Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
XX Schistosoma. The immunomodulatory sequences are used to screen for human  
XX immunostimulatory activity by incubating macrophage cells and the  
XX oligonucleotide, and determining the relative amount of Th1-biased  
XX cytokines in the supernatant. Sequences AAV80104 to AAV80116 represent  
XX cytochromes that were tested for immunostimulatory activity. These  
XX were used in experiments for the stimulation of cytokine production and  
XX were found to lack immunostimulatory activity. The invention provides  
XX specific claimed examples (AAV80096-103) of immunomodulatory sequences.

XX  
SQ Sequence 22 BP; 5 A; 7 C; 4 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 20; Length 22;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGAGATGA 20  
 |||||  
 DB 15 GAACGTTGAGATGA 1

## RESULT 9

AAV80096  
 ID AAV80096 standard; DNA; 22 BP.

AAV80096;

DT 12-MAR-1999 (first entry)

DE Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
 KW ISS; cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
 KW B. pertussis; malaria; plasmodia; leishmania; Trypanosoma; Schistosoma.  
 OS Synthetic.

XX WO9855495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

PT Immunostimulatory oligonucleotides regulate the immune system - and  
 PT contain an immune-stimulating octanucleotide sequence; for treating  
 PT cancer, allergic and infectious diseases

XX Claim 7, Page 29; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCC,  
 CC GACGTTCC, and GACGTTCC. The immunomodulatory sequences are used to treat  
 CC patients needing immune regulation, such as those suffering from cancer,  
 CC an allergic disease and asthma. They are also used to prevent infectious  
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
 CC Bordetella pertussis, malarial plasmodia, leishmania, Trypanosoma and  
 CC Schistosoma. The immunomodulatory sequences are used to screen for human  
 CC immunostimulatory activity by incubating macrophage cells and the  
 CC oligonucleotide; and determining the relative amount of Th1-biased  
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
 CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;

Query Match 71.4%; Score 15; DB 20; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGAGATGA 20  
 |||||  
 DB 8 GAACGTTGAGATGA 22

## RESULT 10

AAV80097

ID AAV80097 standard; DNA; 22 BP.

XX

AC AAV80097;

XX 12-MAR-1999 (first entry)

DE Immunomodulatory oligo comprising an ISS sequence.

KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
 KW ISS; cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
 KW B. pertussis; malaria; plasmodia; leishmania; Trypanosoma; Schistosoma.

OS Synthetic.

XX WO9855495-A2.

XX 10-DEC-1998.

XX 05-JUN-1998; 98WO-US11578.

XX 06-JUN-1997; 97US-0048793.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Dina D, Roman M, Schwartz D;

XX WPI; 1999-059898/05.

PT Immunostimulatory oligonucleotides regulate the immune system - and  
 PT contain an immune-stimulating octanucleotide sequence; for treating  
 PT cancer, allergic and infectious diseases

XX Claim 5, Page 29; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise  
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCC,  
 CC GACGTTCC, and GACGTTCC. The immunomodulatory sequences are used to treat  
 CC patients needing immune regulation, such as those suffering from cancer,  
 CC an allergic disease and asthma. They are also used to prevent infectious  
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
 CC Bordetella pertussis, malarial plasmodia, leishmania, Trypanosoma and  
 CC Schistosoma. The immunomodulatory sequences are used to screen for human  
 CC immunostimulatory activity by incubating macrophage cells and the  
 CC oligonucleotide; and determining the relative amount of Th1-biased  
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
 CC specific claimed examples of such immunomodulatory oligonucleotides.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 20; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGAGATGA 20  
 |||||  
 DB 8 GAACGTTGAGATGA 22

## RESULT 11

AAV80102

ID AAV80102 standard; DNA; 22 BP.

XX AAV80102;

DT 12-MAR-1999 (first entry)

DE Immunomodulatory oligo comprising an ISS sequence.

KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
 KW ISS; cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
 KW B. pertussis; malaria; plasmodia; leishmania; Trypanosoma; Schistosoma.

```

XX OS Synthetic.
XX FH Key
XX FT modified_base 11
XX FT /tag= a
XX FT /note= "5-bromocytosine"
XX PN MO9855495-A2.
XX PD 10-DEC-1998.
XX PF 05-JUN-1998; 98WO-US11578.
XX PR 06-JUN-1997; 97US-0048793.
XX PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX PI Dina D, Roman M, Schwartz D;
XX DR MPI, 1999-059898/05.
XX PT Immunostimulatory oligonucleotides regulate the immune system - and
XX PT contain an immune-stimulating octanucleotide sequence; for treating
XX PT cancer, allergic and infectious diseases
XX PS Claim 23; Page 30; 63pp; English.
XX CC The invention relates to immunomodulatory oligonucleotides that comprise
XX CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
XX CC sequences are selected from the group consisting of AACGTTCC, AACGTTGC,
XX CC GAGCTTCC, and GAGCTTCG. The immunomodulatory sequences are used to treat
XX CC patients needing immune regulation, such as those suffering from cancer,
XX CC an allergic disease and asthma. They are also used to prevent infectious
XX CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
XX CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
XX CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
XX CC Schistosoma. The immunomodulatory sequences are used to screen for human
XX CC immunostimulatory activity by incubating macrophage cells and the
XX CC oligonucleotide; and determining the relative amount of Th1-biased
XX CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
XX CC specific claimed examples of such immunomodulatory oligonucleotides.
XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
XX
XX Query Match 71.4%; Score 15; DB 20; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 19;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 GAACGTTGAGATGA 20
XX DB 8 GAACGTTGAGATGA 22
XX
XX RESULT 12
XX ID AAV80103 standard; DNA; 22 BP.
XX AC AAV80103;
XX XX
XX DT 12-MAR-1999 (first entry)
XX DE Immunomodulatory oligo comprising an ISS sequence.
XX XX
XX KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
XX KW ISS; cancer; allergy; asthma; hepatitis B infection; papillomavirus;
XX KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
XX KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX OS Synthetic.
XX XX
XX Key modified_base 11 Location/Qualifiers

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XX FT /tag= a
XX FT /note= "5-bromocytosine"
XX PN MO9855495-A2.
XX PD 10-DEC-1998.
XX PF 05-JUN-1998; 98WO-US11578.
XX PR 06-JUN-1997; 97US-0048793.
XX PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX PI Dina D, Roman M, Schwartz D;
XX DR MPI, 1999-059898/05.
XX PT Immunostimulatory oligonucleotides regulate the immune system - and
XX PT contain an immune-stimulating octanucleotide sequence; for treating
XX PT cancer, allergic and infectious diseases
XX PS Claim 24; Page 30; 63pp; English.
XX CC The invention relates to immunomodulatory oligonucleotides that comprise
XX CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
XX CC sequences are selected from the group consisting of AACGTTCC, AACGTTGC,
XX CC GAGCTTCC, and GAGCTTCG. The immunomodulatory sequences are used to treat
XX CC patients needing immune regulation, such as those suffering from cancer,
XX CC an allergic disease and asthma. They are also used to prevent infectious
XX CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
XX CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
XX CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
XX CC Schistosoma. The immunomodulatory sequences are used to screen for human
XX CC immunostimulatory activity by incubating macrophage cells and the
XX CC oligonucleotide; and determining the relative amount of Th1-biased
XX CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
XX CC specific claimed examples of such immunomodulatory oligonucleotides.
XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
XX
XX Query Match 71.4%; Score 15; DB 20; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 19;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 GAACGTTGAGATGA 20
XX DB 8 GAACGTTGAGATGA 22
XX
XX RESULT 13
XX ID AAC64051 standard; DNA; 22 BP.
XX AC AAC64051;
XX XX
XX DT 15-FEB-2001 (first entry)
XX DE Immunostimulatory CpG phosphorothioate oligodeoxynucleotide.
XX XX
XX KW CpG oligodeoxynucleotide; phosphorothioate; immunostimulatory; ISS ODN;
XX KW enhanced antigen presentation; antigen-presenting cell; APC;
XX KW T-cell activation; tumour cell; tumour antigen; cancer immunotherapy;
XX KW vaccine; ss.
XX OS Synthetic.
XX XX
XX PN WO200062787-A1.
XX PD 26-OCT-2000.
XX PF 11-APR-2000; 2000WO-US09664.
XX PR 15-APR-1999; 99US-0292278.

```

XX (REGC ) UNIV CALIFORNIA.  
 XX  
 XX Raz E, Martin-Orozco E;  
 XX  
 XX WPI; 2000-679548/66.  
 XX  
 XX Enhancing antigen-presentation capabilities of T-cells for cancer  
 PT immunotherapy, by contacting cells with an immunostimulatory  
 PT oligonucleotide -  
 XX  
 XX Example I; Page 18; 42pp; English.  
 XX  
 CC The invention relates to a method of inducing activation of T-cells  
 CC to respond to an antigen, comprising contacting antigen-presenting cells  
 CC (APC) with an immunostimulatory oligodeoxynucleotide (ISS-ODN). The APCs  
 CC thus treated have enhanced antigen presenting capabilities compared to  
 CC antigen-activated APCs. APCs with enhanced antigen-presentation  
 CC capabilities then present the antigen to T-cells. The method is useful  
 CC for cancer immunotherapy. The ISS-ODN is used to enhance the tumour  
 CC antigen presenting capacity of tumour cells, thereby inducing T-cell  
 CC activation, and is therefore useful for treating tumours. Additionally,  
 CC tumour cells treated with an ISS-ODN ex vivo are useful as vaccines.  
 CC ISS-ODN treated APCs are induced to take up antigen through upregulation  
 CC of Fe-receptor expression, to present antigen through upregulation of  
 CC major histocompatibility complex (MHC) Class I and II expression and  
 CC CD40 expression, to produce co-stimulatory factors (B7 and CD40), to  
 CC provide cell-to-cell adhesion through upregulation of intercellular  
 CC adhesion molecule (ICAM) expression, and to increase Th1 stimulatory  
 CC cytokine production, all at levels greater than that achieved through  
 CC contact of APC with antigen alone. The present sequence represents  
 CC a phosphorothioate Cpg ISS-ODN used in the exemplifications of the  
 CC invention.  
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;  
 QY Query Match 71.4%; Score 15; DB 21; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 6 GAACGTTGAGATGA 20  
 8 GAACGTTGAGATGA 22  
 RESULT 14  
 AAA96253  
 ID AAA96253 standard; DNA; 22 BP.  
 AC AAA96253;  
 XX  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX  
 DE Sequence of a stabilised oligonucleotide with antitumour activity.  
 XX  
 XX Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;  
 KW glioblastoma; medulloblastoma; neuroblastoma; carcinoma; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200056342-A2.  
 XX  
 XX 28-SEP-2000.  
 XX  
 XX 17-MAR-2000; 2000WO-FR00676.  
 XX  
 XX 19-MAR-1999; 99FR-0003433.  
 PA (ASSI-) ASSISTANCE PUBLIQUE HOPITALUX PARIS.  
 PA (INRM) INST NAT SANTE & RECH MEDICALE.  
 XX  
 XX Carpenter A;  
 XX

DR WPI; 2000-602192/57.  
 XX  
 XX Use of stabilized oligonucleotides as antitumor agents, particularly  
 PT against nervous system tumors, have optimal activity and are not toxic  
 PT -  
 XX  
 XX Example 2; Page 16; 57pp; French.  
 XX  
 CC The present sequence represents a stabilised oligonucleotide which has  
 CC antitumour activity. The oligonucleotide comprises an octamer motif  
 CC of the type 5'-purine-purine-CG-pyrimidine-pyrimidine-X-X-3', where  
 CC the pair X-X is AT, AA, CT or TT. The oligonucleotides are  
 CC immunostimulatory, and are not toxic. They may be adapted for use in  
 CC animals or humans. The stabilised oligonucleotides are used for  
 CC treating tumours, of any type and any degree of anaplasia, particularly  
 CC human tumours in the peripheral or central nervous systems, specifically  
 CC glioblastomas, medulloblastomas, neuroblastomas, melanomas or carcinomas.  
 XX  
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;  
 QY Query Match 71.4%; Score 15; DB 21; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 6 GAACGTTGAGATGA 20  
 8 GAACGTTGAGATGA 22  
 RESULT 15  
 AAA90458  
 ID AAA90458 standard; DNA; 22 BP.  
 AC AAA90458;  
 XX  
 XX  
 DT 10-JAN-2001 (first entry)  
 XX  
 DE Cpg adjuvant oligonucleotide, SEQ ID NO:19.  
 XX  
 KW Cpg oligonucleotide; Cpg motif; adjuvant; microdroplet emulsion;  
 KW microemulsion; adsorbent microparticle; vaccine; Th1 immune response;  
 KW viral infection; bacterial infection; parasitic infection; HCV; HBV;  
 KW hepatitis C virus; hepatitis B virus; herpes simplex virus; HSV; HIV;  
 KW human immunodeficiency virus; cytomegalovirus; CMV; influenza virus;  
 KW rabies virus; cholera; diphtheria; tetanus; pertussis;  
 KW Helicobacter pylori; Haemophilus influenzae; malaria; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200050006-A2.  
 XX  
 XX 31-AUG-2000.  
 PD  
 XX  
 PF 09-FEB-2000; 2000WO-US03331.  
 XX  
 XX 26-FEB-1999; 99US-0121858.  
 PR 29-JUL-1999; 99US-0146391.  
 PR 28-OCT-1999; 99US-0161997.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 XX  
 XX O'Hagan D, Olt GS, Donnelly J, Kazaz J, Ugozzoli M, Singh M;  
 PI Barackman J;  
 XX  
 XX WPI; 2000-587123/55.  
 XX  
 XX Microemulsion having an adsorbent surface comprising a microdroplet  
 PT emulsion consisting of a metabolizable oil and an emulsifying agent  
 PT which is a detergent, useful as a vaccine to treat bacterial, viral,  
 PT and parasitic infection -  
 XX  
 PS Claim 17; Page 40; 95pp; English.  
 XX

CC The invention relates to a microdroplet emulsion (microemulsion) with an  
CC adsorbent surface, and which comprises a metabolizable oil and an  
CC emulsifying agent (a detergent). It also relates to a composition  
CC comprising the microemulsion and a microparticle with an adsorbent  
CC surface, where the microparticle comprises a polymer selected from a  
CC poly(alpha-hydroxy acid), a polyhydroxy butyric acid, a  
CC polycaprolactone, a polyorthoester, a polyamide, and a  
CC polycyanoacrylate, and a second detergent. The surface of the  
CC microparticles efficiently adsorb biologically active macromolecules such  
CC as DNA, polypeptides, antigens, hormones, pharmaceuticals, enzymes,  
CC mediators of transcription or translation, metabolic intermediates and  
CC adjuvants. Additionally, a second biologically active molecule may be  
CC encapsulated within the microparticle. The microemulsion can be used in  
CC methods of immunising a host animal, particularly a human, against a  
CC viral, bacterial or parasitic infection, and in methods of increasing a  
CC Th1 immune response. The microemulsions (having the appropriate antigens  
CC adsorbed) may be particularly used as vaccines for hepatitis C virus  
CC (HCV), hepatitis B virus (HBV), herpes simplex virus (HSV), human  
CC immunodeficiency virus (HIV), cytomegalovirus (CMV), influenza virus, and  
CC rabies virus; the bacteria which cause cholera, diphtheria, tetanus and  
CC pertussis; Helicobacter pylori and Haemophilus influenzae; and  
CC malaria-causing parasites. Sequences AAA80447-A90467 represent Th1  
CC lymphocyte stimulating oligonucleotides containing at least one Cpg motif  
CC which are claimed for use as adjuvants in the compositions of the  
CC invention.

CC SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 21; Length 22;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGAGATGA 20  
Db 8 GAACGTTGAGATGA 22

#### RESULT 16

AAA14467  
ID AAA14467 standard; DNA; 22 BP.

AC AAA14467;

DT 21-AUG-2000 (first entry)

DB Immunostimulatory oligonucleotide (ISS-ODN) DY1018.

KW Immunostimulatory oligonucleotide; adjuvant; mucosal immunity;  
KW secretory immunoglobulin A production; sIgA; Th1 phenotype; ds.  
XX  
OS Synthetic.

PN WO20020039-A1.

PD 13-APR-2000.

PF 15-SEP-1999; 99WO-US21203.

PR 05-OCT-1998; 98US-0167039.

PA (REGC) UNIV CALIFORNIA.

PI Raz E, Horner AA, Carson DA;

DR WPI; 2000-303647/26.

PT Immunostimulatory oligonucleotide adjuvant induces mucosal immunity to  
PT an antigen in a mammalian host through production of secretory  
PT immunoglobulin A -

PS Claim 8; Page 21; 64pp; English.

XX The invention relates to a method of inducing mucosal immunity to an

CC antigen in a mammalian host, including the the production of secretory  
CC immunoglobulin A (sIgA). Immune protection in the mucosa (the principal  
CC site of entry of most foreign antigens) is mediated by mucosa-associated  
CC lymphoid tissue, epithelial and distinct B-cell, T-cell and accessory  
CC cell sub-populations. The primary immune response which characterises  
CC the induction of mucosal immunity to an antigen is sIgA production by  
CC activated B-cells. The method comprises introducing an immunostimulatory  
CC oligonucleotide (ISS-ODN) and the antigen into host mucosa, where the  
CC ISS-ODN includes a core nucleotide sequence. The core nucleotide  
CC sequence is 5'-Purine-Purine-C-G-Pyrimidine-Pyrimidine-3', specific  
CC examples of which are AACGT, AGCCTC and GACGT (SEQ ID Nos 1-3). A  
CC specific example of an ISS-ODN is DY1018 (AAA14467). The ISS-ODN is used  
CC as an adjuvant with an antigen for stimulating mucosal immunity. The  
CC level of sIgA production induced in the host is at least 3 times the  
CC magnitude of sIgA production achievable in response to introduction of  
CC antigen alone into the mucosal tissue and is equivalent or greater than  
CC the magnitude of sIgA production achievable in response to introduction  
CC of the antigen and cholera toxin adjuvant into the mucosal tissue. The  
CC host immune response is stimulated to antigen specific IgA production,  
CC biased towards the Th1 phenotype while antigen-induced IgE production is  
CC avoided. The adjuvant has little or no known toxicity in mammals and its  
CC efficacy is comparable to that of cholera toxin which is used as a  
CC mucosal adjuvant. The present sequence represents the immunostimulatory  
CC oligonucleotide DY1018.

CC SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 21; Length 22;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGAGATGA 20  
Db 8 GAACGTTGAGATGA 22

#### RESULT 17

AAA38065  
ID AAA38065 standard; DNA; 22 BP.

AC AAA38065;

DT 24-AUG-2000 (first entry)

DB Immunostimulatory sequence (ISS) #1.

KW Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;  
KW gp120; human immunodeficiency virus; HIV; immune response; infection;  
XX development; ss.  
XX  
OS Synthetic.

PN WO20021556-A1.

PD 20-APR-2000.

PF 08-OCT-1999; 99WO-US23677.

PR 09-OCT-1998; 98US-0103733.

PR 07-OCT-1999; 99US-0415186.

PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

PI Tighe H, Raz E, Schwartz D, Takabayashi K;

DR WPI; 2000-317846/27.

PT Anti-HIV composition comprises immunostimulatory polynucleotides and  
PT HIV glycoprotein gp120 useful for modulating, stimulating an immune  
PT response against HIV in an HIV infected individual -

PS Claim 3; Page 16; 65pp; English.

XX



CC The present invention relates to an immunostimulatory composition  
 CC comprising a human immunodeficiency virus (HIV) antigen, and an  
 CC immunomodulatory polynucleotide comprising an immunostimulatory sequence  
 CC (ISS). This sequence represents an ISS that can be used in the  
 CC composition. An immunostimulatory composition which comprises a gp120  
 CC conjugated to an immunomodulatory polynucleotide, or is proximately  
 CC associated to it and not conjugated, is used for modulating or  
 CC stimulating a specific immune response against gp120 in an individual by  
 CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It  
 CC is also used for suppressing or delaying development of HIV infection in  
 CC an individual infected with HIV or an individual at risk of infection  
 CC with HIV, respectively. It is also used for treating an individual  
 CC infected with HIV in need of immune modulation.

CC Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 21; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
 |||||  
 DB 8 GAACGTCGAGATGA 22

RESULT 18

AAA38066  
 ID AAA38066 standard; DNA; 22 BP.

AC AAA38066;

DT 24-AUG-2000 (first entry)

DE Immunostimulatory sequence (ISS) #2.

KM Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;  
 KW gp120; human immunodeficiency virus; HIV; immune response; infection;  
 development; ss.

OS Synthetic.

FN WO200021556-A1.

PD 20-APR-2000.

PF 08-OCT-1999; 99WO-US23677.

PR 09-OCT-1998; 98US-0103733.

PR 07-OCT-1999; 99US-0415186.

PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

PI Tighe H, Raz E, Schwartz D, Takabayashi K;

XX WPI; 2000-317846/27.

PT Anti-HIV composition comprises immunostimulatory polynucleotides and  
 PT HIV glycoprotein gp120 useful for modulating, stimulating an immune  
 PT response against HIV in an HIV infected individual -  
 PS Disclosure; Page 16; 65pp; English.

CC The present invention relates to an immunostimulatory composition  
 CC comprising a human immunodeficiency virus (HIV) antigen, and an  
 CC immunomodulatory polynucleotide comprising an immunostimulatory sequence  
 CC (ISS). This sequence represents an ISS that can be used in the  
 CC composition. An immunostimulatory composition which comprises a gp120  
 CC conjugated to an immunomodulatory polynucleotide, or is proximately  
 CC associated to it and not conjugated, is used for modulating or  
 CC stimulating a specific immune response against gp120 in an individual by  
 CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It  
 CC is also used for suppressing or delaying development of HIV infection in  
 CC an individual infected with HIV or an individual at risk of infection

CC with HIV, respectively. It is also used for treating an individual  
 CC infected with HIV in need of immune modulation.

CC Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;

Query Match 71.4%; Score 15; DB 21; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
 |||||  
 DB 8 GAACGTCGAGATGA 22

RESULT 19

AAA38071  
 ID AAA38071 standard; DNA; 22 BP.

AC AAA38071;

DT 24-AUG-2000 (first entry)

DE Immunostimulatory sequence (ISS) #7.

KM Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;  
 KW gp120; human immunodeficiency virus; HIV; immune response; infection;  
 development; ss.

OS Synthetic.

FN WO200021556-A1.

PD 20-APR-2000.

PF 08-OCT-1999; 99WO-US23677.

PR 09-OCT-1998; 98US-0103733.

PR 07-OCT-1999; 99US-0415186.

PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

PI Tighe H, Raz E, Schwartz D, Takabayashi K;

XX WPI; 2000-317846/27.

PT Anti-HIV composition comprises immunostimulatory polynucleotides and  
 PT HIV glycoprotein gp120 useful for modulating, stimulating an immune  
 PT response against HIV in an HIV infected individual -  
 PS Disclosure; Page 17; 65pp; English.

CC The present invention relates to an immunostimulatory composition  
 CC comprising a human immunodeficiency virus (HIV) antigen, and an  
 CC immunomodulatory polynucleotide comprising an immunostimulatory sequence  
 CC (ISS). This sequence represents an ISS that can be used in the  
 CC composition. An immunostimulatory composition which comprises a gp120  
 CC conjugated to an immunomodulatory polynucleotide, or is proximately  
 CC associated to it and not conjugated, is used for modulating or  
 CC stimulating a specific immune response against gp120 in an individual by  
 CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It  
 CC is also used for suppressing or delaying development of HIV infection in  
 CC an individual infected with HIV or an individual at risk of infection  
 CC with HIV, respectively. It is also used for treating an individual  
 CC infected with HIV in need of immune modulation.

CC Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;



Query Match 71.4%; Score 15; DB 21; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 6 GAACGTCGAGATGA 20  
 |||||  
 8 GAACGTCGAGATGA 22  
 Db

RESULT 20  
 AAA8072  
 ID AAA8072 standard; DNA; 22 BP.  
 AC AAA8072;  
 XX  
 XX 24-APR-2000 (first entry)  
 DT  
 XX Immunostimulatory sequence (ISS) #7.  
 DE  
 XX Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;  
 KW gp120; human immunodeficiency virus; HIV; immune response; infection;  
 KW development; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 11  
 FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "5-Bromocytosine"  
 FT modified\_base 15  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "5-Bromocytosine"  
 FT  
 PN WO200021556-A1.  
 XX  
 XX 20-APR-2000.  
 PD  
 XX 08-OCT-1999; 99WO-US23677.  
 XX  
 XX 09-OCT-1998; 98US-0103733.  
 XX PR 07-OCT-1999; 99US-0415186.  
 XX  
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 PA  
 XX  
 XX Tighe H, Raz E, Schwartz D, Takabayashi K;  
 PI WPI; 2000-317846/27.  
 DR  
 XX  
 XX Anti-HIV composition comprises immunostimulatory polynucleotides and  
 PT HIV glycoprotein gp120 useful for modulating, stimulating an immune  
 PT response against HIV in an HIV infected individual  
 PT  
 XX  
 PS Disclosure: Page 17; 65pp; English.  
 XX  
 XX The present invention relates to an immunostimulatory composition  
 CC comprising a human immunodeficiency virus (HIV) antigen, and an  
 CC immunomodulatory polynucleotide comprising an immunostimulatory sequence  
 CC (ISS). This sequence represents an ISS that can be used in the  
 CC composition. An immunostimulatory composition which comprises a gp120  
 CC conjugated to an immunomodulatory polynucleotide, or is proximately  
 CC associated to it and not conjugated, is used for modulating or  
 CC stimulating a specific immune response against gp120 in an individual by  
 CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It  
 CC is also used for suppressing or delaying development of HIV infection in  
 CC an individual infected with HIV or an individual at risk of infection  
 CC with HIV, respectively. It is also used for treating an individual  
 CC infected with HIV in need of immune modulation.  
 CC  
 XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;  
 SQ  
 Query Match 71.4%; Score 15; DB 21; Length 22;

Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 6 GAACGTCGAGATGA 20  
 |||||  
 8 GAACGTCGAGATGA 22  
 Db

RESULT 21  
 AA255876  
 ID AA255876 standard; DNA; 22 BP.  
 AC AA255876;  
 XX  
 XX 10-APR-2000 (first entry)  
 DT  
 XX Immunomodulatory oligonucleotide SEQ ID NO: 1.  
 DE  
 XX Immunomodulation; immunostimulatory sequence; adjuvant;  
 KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;  
 KW asthma; immunosuppression; ss.  
 XX  
 XX Mus musculus.  
 OS  
 XX Synthetic.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1.22  
 FT /\*tag= a  
 FT /note= "Phosphorothioate linkages"  
 FT misc\_feature 9..16  
 FT /\*tag= b  
 FT /note= "Immunostimulatory sequence (ISS)"  
 FT  
 PN WO9962923-A2.  
 XX  
 XX 09-DEC-1999.  
 PD  
 XX  
 XX 04-JUN-1999; 99WO-US12538.  
 XX  
 XX 05-JUN-1998; 98US-0088310.  
 XX PR 01-JUN-1999; 99US-0324191.  
 XX  
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 PA  
 XX  
 XX Schwartz D;  
 PI WPI; 2000-105687/09.  
 DR  
 XX  
 XX Novel immunomodulatory oligonucleotide used to induce a Th1-type immune  
 PT response, e.g. to tumor antigens  
 PT  
 XX  
 PS Example 1; Page 35; 54pp; English.  
 XX  
 XX Sequences AA255876-255877 and AA255880-255886 represent immunomodulatory  
 CC oligonucleotides comprising an immunostimulatory sequence (ISS, e.g.,  
 CC AACGTC, AACGTT, AGCGTC, AGCGCT, AGCGTT, GAGGTC, GAGGTT, GGCGTT,  
 CC AACGTC and GAGGTC). The invention relates to oligonucleotides  
 CC comprising one or more ISSs, where the ISS comprises at least  
 CC one modified cytosine with an electron-withdrawing moiety at  
 CC position C-5 or C-6 of the base. Sequences AA255877 and AA255880-255886  
 CC contain ISSs comprising at least one bromocytosine, whereas sequence  
 CC AA255876 contains an unmodified ISS. The immunomodulatory  
 CC oligonucleotides have an adjuvant-like effect, when formulated with an  
 CC antigen, the oligonucleotides stimulate production of Th1-type cytokines,  
 CC and induce a Th1-type immune response (activation of cytotoxic T cells),  
 CC while simultaneously downregulating the Th2-type response. The Th1  
 CC response is particularly effective for control of viruses and  
 CC intracellular parasites. The immunomodulatory oligonucleotides are used,  
 CC particularly when formulated with an antigen or a facilitator, for  
 CC modulating immune responses. Such compositions may be used in tumor  
 CC therapy, in treatment of allergy (including asthma), for inducing a  
 CC vigorous cellular response (against a virus, bacterium, fungus or  
 CC protozoan), and also in contraceptive vaccines based on sperm antigens.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;  
SQ

Query Match 71.4%; Score 15; DB 21; Length 22;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGAGATGA 20  
|||  
8 GAACGTTGAGATGA 22

## RESULT 22

AAH43338  
ID AAH43338 standard; DNA; 22 BP.

AC AAH43338;

DT 13-DEC-2001 (first entry)

DE Immunomodulatory polynucleotide 1018.

KW ulcerative colitis; Crohn's disease; inflammatory bowel disease;

KW diarrhoea; rectal bleeding; weight loss; colon; weight; lesion; ss.

OS Synthetic.

PN WO200162207-A2.

PD 30-AUG-2001.

PF 22-FEB-2001; 2001WO-US06034.

PR 23-FEB-2000; 2000US-0184256.

PA (REGC ) UNIV CALIFORNIA.

PI Raz E, Rachmilewitz D;

DR WPI; 2001-565393/63.

PT Ameliorating gastrointestinal inflammation e.g. inflammatory bowel  
XX disease involves administering an immunomodulatory nucleic acid -

PS Claim 7; Page 28; 58pp; English.

The sequences given in AAH43338-48 represent immunomodulatory  
XX polynucleotides which may be used to ameliorate inflammation of  
CC the gastrointestinal tract by administering a nucleic acid comprising  
CC one of these sequences. These polynucleotides all comprise an  
CC immunomodulatory nucleotide sequence of 5'-CpG-3' (I). The  
CC nucleotides may be used for ameliorating or reducing gastrointestinal  
CC inflammation e.g. chronic or acute gastrointestinal inflammation,  
CC ulcerative colitis, Crohn's disease caused by inflammatory bowel  
CC disease; diarrhoea, rectal bleeding, weight loss; to reduce colon  
CC weight and colon lesions; to reduce a colonic inflammation. The  
CC immunomodulatory polynucleotides treat inflammatory bowel disease  
CC satisfactorily and effectively and have little or no toxicity even  
CC at a high dosage of 50000 micro-g. They also reduce the risk of  
CC colonic cancer by treating ulcerative colitis.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;  
SQ

Query Match 71.4%; Score 15; DB 22; Length 22;  
Best Local Similarity 100.0%; Pred. No. 19;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGAGATGA 20  
|||  
8 GAACGTTGAGATGA 22

## RESULT 23

AA514664  
ID AA514664 standard; DNA; 22 BP.

AC AA514664;

DT 18-DEC-2001 (first entry)

DE Immunostimulatory sequence, ISS #1.

KW Immunostimulatory sequence; ISS; ds; antiviral; immunogen;

KW respiratory syncytial virus; RSV; influenza virus; rhinovirus;

KW adenovirus; measles virus; mumps virus; parainfluenza virus;

OS Respiratory syncytial virus.

FT Key Location/Qualifiers

FT modified\_base 1..22

FT /tag= a

FT /label= OTHER

PN WO200168116-A2.

PD 20-SEP-2001.

PF 12-MAR-2001; 2001WO-US07839.

PR 10-MAR-2000; 2000US-186683P.

PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

PI Van Nest G;

DR WPI; 2001-607438/69.

PT Suppressing a respiratory syncytial virus infection by administering an  
XX immunostimulatory sequence at the site of infection is useful to  
XX prevent and treat lower respiratory tract viral infections -

PS Claim 5; Page 37; 40pp; English.

The invention relates to suppressing a respiratory syncytial virus (RSV)  
XX infection in an exposed individual, comprising administering a  
CC polynucleotide comprising an immunostimulatory sequence (ISS) comprising  
CC the sequence 5'-C-G-3', where an RSV antigen is not administered.  
CC The invention is used to prevent and treat respiratory syncytial  
CC virus infection of the lower respiratory tract and other viruses  
CC including influenza virus, rhinovirus, adenovirus, measles virus, mumps  
CC virus, parainfluenza virus, rubella virus, poxvirus, parvovirus,  
CC hantavirus and varicella virus. A kit for carrying out  
CC the administration is also included. Unlike the prior art antiviral agent  
CC ribavirin, which is a potential teratogen, the invention provides a  
CC treatment which does not carry unacceptable side effects. Other prior art  
CC medicaments treat the symptoms only, whilst the invention treats the  
CC infection. The present sequence is an ISS of the invention.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;  
SQ

Query Match 71.4%; Score 15; DB 22; Length 22;  
Best Local Similarity 100.0%; Pred. No. 19;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGAGATGA 20  
|||  
8 GAACGTTGAGATGA 22

## RESULT 24

AA514665

```

ID  AA514665 standard; DNA; 22 BP.
XX
AC  AA514665;
XX
DT  18-DEC-2001 (first entry)
XX
DE  Immunostimulatory sequence, ISS #2.
XX
KM  Immunostimulatory sequence; ISS; ds; antiviral; immunogen;
KM  respiratory syncytial virus; RSV; influenza virus; rhinovirus;
KM  adenovirus; measles virus; mumps virus; parainfluenza virus;
KM  rubella virus; poxvirus; parvovirus; hantavirus; varicella virus.
XX
OS  Respiratory syncytial virus.
OS  Synthetic.
XX
FN  WO200168116-A2.
XX
PD  20-SEP-2001.
XX
PF  12-MAR-2001; 2001WO-US07839.
XX
PR  10-MAR-2000; 2000US-188583P.
XX  09-MAR-2001; 2001US-0802686.
XX
PA  (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI  Van Nest G;
XX
DR  WPI; 2001-607438/69.
XX
PT  Suppressing a respiratory syncytial virus infection by administering an
PT  immunostimulatory sequence at the site of infection is useful to
PT  prevent and treat lower respiratory tract viral infections -
XX
PS  Disclosure; Page 15; 40pp; English.
XX
XX  The invention relates to suppressing a respiratory syncytial virus (RSV)
CC  infection in an exposed individual, comprising administering a
CC  polynucleotide comprising an immunostimulatory sequence (ISS) comprising
CC  the sequence 5'-C, G-3', where an RSV antigen is not administered.
CC  The invention is used to prevent and treat respiratory syncytial
CC  virus infection of the lower respiratory tract and other viruses
CC  including influenza virus, rhinovirus, adenovirus, measles virus, mumps
CC  virus, parainfluenza virus, rubella virus, poxvirus, parvovirus,
CC  hantavirus and varicella virus. A kit for carrying out
CC  the administration is also included. Unlike the prior art antiviral agent
CC  ribavirin, which is a potential teratogen, the invention provides a
CC  treatment which does not carry unacceptable side effects. Other prior art
CC  medicaments treat the symptoms only, whilst the invention treats the
CC  infection. The present sequence is an ISS of the invention.
XX
SQ  Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;

Query Match      71.4%; Score 15; DB 22; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      6 GAACGTTGAGATGA 20
        |||||
        8 GAACGTTGAGATGA 22
DB

```

```

KM  Immunomodulatory; immunostimulatory; Th1-type immune response;
KM  Th2-type immune response; interferon; idiopathic pulmonary fibrosis;
KM  viral infection; phosphorothioate; ss.
XX
OS  Synthetic.
XX
FH  Key
XX  modified_base 1..22
XX  Location/Qualifiers
XX  FT 1..22
XX  FT /+tag= a
XX  FT /mod_base= "OTHER"
XX  FT /note= "Phosphorothioate oligonucleotide"
XX
PN  WO200168143-A2.
XX
PD  20-SEP-2001.
XX
PF  12-MAR-2001; 2001WO-US07843.
XX
PR  10-MAR-2000; 2000US-0188557.
XX  09-MAR-2001; 2001US-0802376.
XX
PA  (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
PI  Van Nest G, Tuck S;
XX
DR  WPI; 2001-582389/65.
XX
PT  Immunomodulatory polynucleotide/microcarrier complexes comprise an
PT  immunostimulatory sequence containing polynucleotide linked to a
PT  nonbiodegradable microcarrier -
XX
PS  Claim 11; Page 49; 61pp; English.
XX
XX  The present invention relates to immunomodulatory polynucleotide/
CC  microcarrier complexes. The complexes comprise an immunostimulatory
CC  sequence (ISS), e.g. the present sequence, linked to a nonbiodegradable
CC  microcarrier provided that if the microcarrier is gold, latex or magnetic
CC  then the linkage is not biotin/avidin. The complex is useful for
CC  modulating an immune response (especially stimulating a Th1-type response
CC  or suppressing a Th2-type response), increasing interferon-gamma
CC  (especially in a patient suffering from idiopathic pulmonary fibrosis),
CC  increasing interferon-alpha (especially in patients suffering from viral
CC  infection) and reducing levels of IgE.
XX
SQ  Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match      71.4%; Score 15; DB 22; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      6 GAACGTTGAGATGA 20
        |||||
        8 GAACGTTGAGATGA 22
DB

```

```

RESULT 25
AAH75992
ID  AAH75992 standard; DNA; 22 BP.
XX
AC  AAH75992;
XX
DT  15-NOV-2001 (first entry)
XX
DE  Immunomodulatory oligonucleotide #1.
XX

```

```

RESULT 26
AAH75993
ID  AAH75993 standard; DNA; 22 BP.
XX
AC  AAH75993;
XX
DT  15-NOV-2001 (first entry)
XX
DE  Immunomodulatory oligonucleotide #2.
XX
KM  Immunomodulatory; immunostimulatory; Th1-type immune response;
KM  Th2-type immune response; interferon; idiopathic pulmonary fibrosis;
KM  viral infection; ss.
XX
OS  Synthetic.
XX
PN  WO200168143-A2.
XX

```

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PD 20-SEP-2001.
XX
XX 12-MAR-2001; 2001WO-US07843.
XX
XX 10-MAR-2000; 2000US-0188557.
XX
XX 09-MAR-2001; 2001US-0802376.
XX
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX Van Nest G, Tuck S;
XX
XX WPI, 2001-582389/65.
XX
XX Immunomodulatory polynucleotide/microcarrier complexes comprise an
XX immunostimulatory sequence containing polynucleotide linked to a
XX nonbiodegradable microcarrier -
XX
XX PS Disclosure; Page 18; 61pp; English.
XX
XX The present invention relates to immunomodulatory polynucleotide/
XX microcarrier complexes. The complexes comprise an immunostimulatory
XX sequence (ISS), e.g. the present sequence, linked to a nonbiodegradable
XX microcarrier provided that if the microcarrier is gold, latex or magnetic
XX then the linkage is not biotin/avidin. The complex is useful for
XX modulating an immune response (especially stimulating a Th1-type response
XX or suppressing a Th2-type response), increasing interferon-gamma
XX (especially in a patient suffering from idiopathic pulmonary fibrosis),
XX increasing interferon-alpha (especially in patients suffering from viral
XX infection) and reducing levels of IgE.
XX
XX SQ Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;
XX
XX Query Match 71.4%; Score 15; DB 22; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 19;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 6 GAACGTCGAGATGA 20
DB 8 GAACGTCGAGATGA 22
XX
XX RESULT 27
XX AAH42533
XX ID AAH42533 standard; DNA; 22 BP.
XX
XX AC AAH42533;
XX
XX DT 01-OCT-2001 (first entry)
XX
XX DE Phosphorothioate beta-gal/immunostimulatory oligonucleotide.
XX
XX KW Anaphylactic hypersensitivity; immunomodulatory nucleic acid; vaccine;
XX anaphylaxis-associated symptom; IgE; histamine; phosphorothioate; ss.
XX
XX OS Synthetic.
XX
XX PN WO200145750-A1.
XX
XX PD 28-JUN-2001.
XX
XX PF 20-DEC-2000; 2000WO-US35064.
XX
XX PR 21-DEC-1999; 99US-0171830.
XX
XX PA (REGC ) UNIV CALIFORNIA.
XX
XX PI Raz E, Horner AA;
XX
XX DR WPI, 2001-475812/51.
XX
XX PT Reducing risk of anaphylactic hypersensitivity response to an allergen
XX in a subject, by administering an immunomodulating nucleic acid
XX molecule comprising a specific sequence -

```

```

XX
XX Example 1; Page 22; 39pp; English.
XX
XX The specification describes a method for reducing a symptom associated
XX with anaphylactic hypersensitivity or risk of anaphylactic response in
XX a subject. The method comprises administering to an individual a
XX nucleic acid molecule comprising an immunomodulatory nucleic acid
XX molecule (INA) comprising the sequence 5'-C-G-3' to reduce
XX anaphylaxis-associated symptom. The method is useful for reducing a
XX symptom associated with anaphylactic hypersensitivity, including
XX elevated IgE level, elevated histamine level, constriction of the
XX airways and difficult breathing which can lead to anaphylactic reaction
XX or anaphylactic shock, thereby reducing the risk of death. The present
XX sequence represents a beta-gal/immunostimulatory sequence, which was
XX used as a vaccine to protect against the development of anaphylactic
XX hypersensitivity.
XX
XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
XX
XX Query Match 71.4%; Score 15; DB 22; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 19;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 6 GAACGTCGAGATGA 20
DB 8 GAACGTCGAGATGA 22
XX
XX RESULT 28
XX AAH73439
XX ID AAH73439 standard; DNA; 22 BP.
XX
XX AC AAH73439;
XX
XX DT 01-OCT-2001 (first entry)
XX
XX DE Immunomodulatory nucleic acid.
XX
XX KW G3PDH gene; immunomodulatory oligonucleotide; infection; mycobacterium;
XX intracellular pathogen; anti-pathogenic; ss.
XX
XX OS Unidentified.
XX
XX PN WO200155341-A2.
XX
XX PD 02-AUG-2001.
XX
XX PF 30-JAN-2001; 2001WO-US03029.
XX
XX PR 31-JAN-2000; 2000US-0179353.
XX
XX PA (REGC ) UNIV CALIFORNIA.
XX
XX PI Raz E, Kornbluth R, Catanzaro A, Hayashi T, Carson DA;
XX
XX DR WPI, 2001-483234/52.
XX
XX PT Treating infection of intracellular pathogen e.g., Mycobacterium, in a
XX subject, involves administering immunomodulatory nucleic acid molecule
XX to inhibit intracellular replication of intracellular pathogen -
XX
XX PS Examples; Page 26; 54pp; English.
XX
XX CC The present invention describes a method of treating an infection caused
XX by an intracellular pathogen, involving administering to the patient an
XX immunomodulatory nucleic acid and an anti-pathogenic agent. This is
XX particularly useful in the treatment of mycobacterial infections. The
XX present sequence is an immunomodulatory nucleic acid described in the
XX exemplification of the invention.
XX
XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
XX
XX Query Match 71.4%; Score 15; DB 22; Length 22;

```

[illegible]

	CC	proteins and affect cellular metabolism, cell viability or virus replication.
	CC	(I) is useful for delivering any protein of interest, including therapeutically useful proteins (e.g. tumour suppressor
	CC	proteins, cytic fibrosis transmembrane regulator (CFTR), adenosine deaminase (ADA), hexosaminidase A, peptides, wild type protein
	CC	counterparts of mutant proteins and cell surface receptors) such as those for cytokines (e.g., interleukin, interferons, colony stimulating factors) and peptide hormones.
	CC	The present sequence represents a peptide nucleic acid (PNA) oligonucleotide which is used in an example from the present invention for intracellular delivery of proteins.
SQ	XX	Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
	Dy	Query Match            71.4%; Score 15; DB 22, Length 22; Best Local Similarity 100.0%; Pred. No. 19; Matches     15; Conservative     0; Mismatches       0; Indels       0; Gaps      0.
Dd	8	GACGTCGAGATGA 20       GAACGTCGAGATGA 22
<b>RESULT 30</b>		
AH41573	ID	AH41573 standard; DNA; 22 BP.
AA41573;	AC	
24-AUG-2001	DT	(first entry)
Immunostimulatory sequence (ISS) SEQ ID NO:1.	DE	
Immunostimulatory sequence; ISS; immunomodulatory; immune response; antigen; antiallergic; modulation; Th1 lymphocyte stimulation; allergy; Th1-associated cytokine; Th2 lymphocyte suppression; cytokine; ss.	KW	
Synthetic.	OS	
WO200135991-A2.	PN	
25-MAY-2001.	PD	
15-NOV-2000; 2000MO-US31385.	PX	
15-NOV-1999; 99US-0165467.	PR	
14-NOV-2000; 2000US-0713136.	PR	
(DYNA-) DYNAX TECHNOLOGIES CORP.	PA	
Tuck S, Van Nest G;	PI	
WPI; 2001-329209/34.	PT	
Populations of conjugate molecules comprising polynucleotide immunostimulatory sequences polynucleotides and antigens, useful for controlling immune responses -	PP	
Example 1, Page 30; 97bp; English.	PS	
XX	XX	The present invention describes immunomodulatory populations ((I) and ((II)) of conjugate molecules (Cm) comprising immunostimulatory sequences ((SS) of polynucleotides and antigens. The extent of conjugation affects the immunological properties (e.g. the extent of antigen-specific antibody formation, including Th1-associated antibody formation) so the conjugates are used for altering the type and extent of immune response. ((I) and ((II)) have immunomodulatory, immunosuppressive and anti-allergic activities, and can be used in the modulation of immune responses via the stimulation of Th1 lymphocytes and Th1-associated cytokines, and CC suppression of Th2 lymphocytes and cytokines. The populations ((I) and ((II)) of conjugate molecules may be used for modulating immune responses in individuals e.g. for the treatment of an allergic condition. ((I) and ((II)) may be used to modulate immune responses and therefore prevent potentially harmful reactions to antigens. The present sequence

CC represents an ISS polynucleotide which is used in the exemplification  
 CC of the present invention.

SC Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 22; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
 |||||  
 DB 8 GAACGTCGAGATGA 22

RESULT 31  
 AAH41574  
 ID AAH41574 standard; DNA; 22 BP.

AC AAH41574;  
 XX  
 DT 24-AUG-2001 (first entry)

XX Immunostimulatory sequence (ISS) SEQ ID NO:2.

XX Immunostimulatory sequence; ISS; immunomodulatory; immune response;  
 KW antigen; antiallergic; modulation; Th1 lymphocyte stimulation; allergy;  
 KW Th1-associated cytokine; Th2 lymphocyte suppression; cytokine; ss.

XX Synthetic.

XX WO200135991-A2.

XX 25-MAY-2001.

XX 15-NOV-2000; 2000WO-US31385.

XX 15-NOV-1999; 99US-0165467.

XX 14-NOV-2000; 2000US-0713136.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Tuck S, Van Nest G;

XX WPI; 2001-329209/34.

XX Populations of conjugate molecules comprising polynucleotide  
 PT immunostimulatory sequences polynucleotides and antigens, useful for  
 PT controlling immune responses -

XX Disclosure; Page 30; 97pp; English.

XX The present invention describes immunomodulatory populations ((i) and  
 CC ((ii)) of conjugate molecules (CMs) comprising immunostimulatory sequences  
 CC ((ISS)) of polynucleotides and antigens. The extent of conjugation affects  
 CC the immunological properties (e.g. the extent of antigen-specific  
 CC antibody formation, including Th1-associated antibody formation) so the  
 CC conjugates are used for altering the type and extent of immune response.  
 CC ((i) and ((ii)) have immunomodulatory, immunosuppressive and antiallergic  
 CC activities, and can be used in the modulation of immune responses via  
 CC suppression of Th1 lymphocytes and Th1-associated cytokines, and  
 CC ((ii)) of conjugate molecules may be used for modulating immune responses  
 CC in individuals e.g. for the treatment of an allergic condition. ((i) and  
 CC ((ii)) may be used to modulate immune responses and therefore prevent  
 CC potentially harmful reactions to antigens. The present sequence  
 CC represents an ISS polynucleotide which is used in the exemplification  
 CC of the present invention.

XX Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;

Query Match 71.4%; Score 15; DB 22; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
 |||||  
 DB 8 GAACGTCGAGATGA 22

RESULT 32  
 AAH20403  
 ID AAH20403 standard; DNA; 22 BP.

AC AAH20403;

XX 03-AUG-2001 (first entry)

XX Cpg motif containing oligonucleotide SEQ ID #21.

XX Immune system stimulator; Cpg motif; Cpg receptor; Cpg-R; antibacterial;  
 KW immune response; vaccine adjuvant; tumour immunotherapy; allergy;  
 KW anti-inflammatory; cystic fibrosis; sepsis; heart disease; chlamydia;  
 KW inflammatory bowel disease; arthritis; multiple sclerosis; ss.

XX Unidentified.

XX Key Location/Qualifiers

FT modified\_base 1..22  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate internucleoside linkages"

XX WO200132877-A2.

XX 10-MAY-2001.

XX 01-NOV-2000; 2000WO-USA1735.

XX 02-NOV-1999; 99US-0163157.

XX 24-NOV-1999; 99US-0167389.

XX (CHIR ) CHIRON CORP.

XX Mackichan ML;

XX WPI; 2001-343486/36.

XX Novel Cpg receptor and nucleic acid molecule encoding the receptor, for  
 PT modulating immune response and for identifying compounds of therapeutic  
 PT use which bind and/or modulate the activity of the receptor -

XX Example 1; Page 14; 41pp; English.

XX Unmethylated CG dinucleotide sequences are commonly found in bacterial  
 CC DNA, and have been found to stimulate the innate immune system. Natural  
 CC killer and T cells are activated by exposure to oligonucleotides  
 CC containing Cpg motifs. Oligonucleotides containing Cpg motifs can be used  
 CC as adjuvants in vaccines. The present invention relates to a Cpg  
 CC receptor. The Cpg receptor contains a Toll homology domain (THD). The  
 CC Toll receptor family are associated with responses to pathogens. Cpg  
 CC oligonucleotides may act as stimulators of various immune responses. The  
 CC Cpg receptor or cells expressing the receptor are useful for identifying  
 CC a compound which binds to or modulates an activity of the Cpg receptor.  
 CC The compounds are useful in e.g. vaccine adjuvants promoting  
 CC cell-mediated immune responses, antibacterials, (e.g. protection from  
 CC listeria infection), tumour immunotherapy, allergy treatment, (e.g.  
 CC suppressing IgE in human PMC, shifting from Th2 to Th1) and as  
 CC anti-inflammatory agents (e.g. for use in cystic fibrosis, sepsis, heart  
 CC disease, chlamydia, inflammatory bowel disease, arthritis and multiple  
 CC sclerosis). The present sequence represents a Cpg motif containing  
 CC oligonucleotide used in examples demonstrating that Cpg oligonucleotides  
 CC can activate the MAPK pathways and NF-kappaB.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 22; Length 22;

Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
|||  
Db 8 GAACGTCGAGATGA 22

## RESULT 33

AAf77040  
ID AAF77040 standard; DNA; 22 BP.

AC AAF77040;

DT 15-MAY-2001 (first entry)

DE Immunomodulatory DNA.

KV Modulate; immune; antigen; immunostimulatory; ds.

OS Synthetic.

PN WO200112223-A2.

PD 22-FEB-2001.

PE 18-AUG-2000; 2000WO-US22835.

PR 19-AUG-1999; 99US-0149768.

PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

PI Van Nest G;

DR WPI; 2001-211136/21.

XX Modulating immune response to a second antigen in humans involves

PT administering an immunostimulatory polynucleotide comprising an

XX immunostimulatory sequence and a first antigen -

PS Claim 31, Page 15; 63pp; English.

CC The present invention relates to modulating an immune response to

CC a second antigen in an individual, involving

CC administering to the individual an immunomodulatory polynucleotide

CC comprising an immunostimulatory sequence (ISS) and a first antigen.

XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

OY Query Match 71.4%; Score 15; DB 22; Length 22;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 GAACGTCGAGATGA 20  
|||  
8 GAACGTCGAGATGA 22

## RESULT 34

AAf77041  
ID AAF77041 standard; DNA; 22 BP.

AC AAF77041;

DT 15-MAY-2001 (first entry)

DE Immunostimulatory DNA #1.

KV Modulate; immune; antigen; immunostimulatory; ds.

OS Synthetic.

PN WO200112223-A2.

XX 22-FEB-2001.

PE 18-AUG-2000; 2000WO-US22835.

PR 19-AUG-1999; 99US-0149768.

PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

PI Van Nest G;

DR WPI; 2001-211136/21.

XX Modulating immune response to a second antigen in humans involves

PT administering an immunostimulatory polynucleotide comprising an

XX immunostimulatory sequence and a first antigen -

PS Disclosure; Page 15; 63pp; English.

CC The present invention relates to modulating an immune response to

CC a second antigen in an individual, involving

CC administering to the individual an immunomodulatory polynucleotide

CC comprising an immunostimulatory sequence (ISS) and a first antigen.

XX SQ Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;

OY Query Match 71.4%; Score 15; DB 22; Length 22;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 GAACGTCGAGATGA 20  
|||  
8 GAACGTCGAGATGA 22

## RESULT 35

AAf29800  
ID AAF29800 standard; DNA; 22 BP.

AC AAF29800;

DT 12-APR-2001 (first entry)

DE Cholera toxin immunostimulatory nucleotide sequence.

KV Immunostimulatory nucleotide sequence; immune response; cancer;

KV antibody production; IFNgamma release; CTL activity; Th1 response;

XX infection; allergy; ds.

XX OS Unidentified.

PN WO200102007-A1.

PD 11-JAN-2001.

PE 30-JUN-2000; 2000WO-US18229.

PR 02-JUL-1999; 99US-0347343.

PA (REGC ) UNIV CALIFORNIA.

PI Raz E, Kobayashi H;

DR WPI; 2001-138066/14.

XX Enhancing immune response against pathogen or antigen associated with

PT infectious diseases, an allergen or cancer, involves administering

PT immunostimulatory nucleotide sequence prior to antigen exposure -

PS Example 1, Page 14; 47pp; English.

CC The present invention describes a method for enhancing an immune response

CC to a substance, comprising administering an immunostimulatory nucleotide

CC sequence to a subject prior to exposure to the substance. This can be  
 CC used to enhance antibody production, IFNgamma release, CTL activity and  
 CC Th1 related effects. The method can be used in the prevention and  
 CC treatment of allergies, cancer and infections.

XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 22; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
 |||||  
 DB 8 GAACGTCGAGATGA 22

RESULT 36  
 AAC82107  
 ID AAC82107 standard; DNA; 22 BP.

XX AAC82107;  
 XX  
 XX 07-MAR-2001 (first entry)

DE Oligonucleotide ODNCT DNA SEQ ID NO 2.

XX Immunogenic; human immunodeficiency virus; immunostimulatory sequence;  
 XX ISS; beta-chemokine; anti-HIV; AIDS; Th1 immune response; primer;  
 XX HIV-specific cytotoxic T lymphocyte response; phosphorothioate; ss.

OS Synthetic.

XX WO200067787-A2.

XX 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US12495.

XX 06-MAY-1999; 99US-0132762.

XX 25-AUG-1999; 99US-0150667.

XX (IMMU-) IMMUNE RESPONSE CORP.

XX Moss RB;

XX WPI; 2001-031804/04.

XX Human immunodeficiency virus (HIV) compositions useful for immunizing  
 XX and inhibiting AIDS in mammals, comprises HIV devoid of outer envelope  
 XX protein and an immunostimulatory nucleic acid sequence -

XX Example 1; Page 26; 64p; English.

XX This invention describes a novel immunogenic composition (I), comprising  
 XX a whole-killed human immunodeficiency virus (HIV) devoid of outer  
 XX envelope, protein gp120, an isolated nucleic acid molecule containing an  
 XX immunostimulatory sequence (ISS) and an adjuvant, which enhances  
 XX beta-chemokine levels in a mammal. The products of the invention have  
 XX anti-HIV activity. (I) is useful for immunizing and for inhibiting AIDS  
 XX in a mammal. The mammal can be a primate such as a human. (HIV  
 XX seronegative or seropositive humans) or a rodent, in particular the  
 XX primate is a pregnant mother or an infant. (I) can induce potent Th1  
 XX immune responses against a broad spectrum of HIV epitopes and provides a  
 XX strong HIV-specific cytotoxic T lymphocyte response.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 22; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
 |||||

DB 8 GAACGTCGAGATGA 22

RESULT 37  
 AAA92377

ID AAA92377 standard; DNA; 22 BP.

XX AAA92377;

XX 12-JAN-2001 (first entry)

DE CG motif and CFA containing oligonucleotide SEQ ID NO:19.

XX

XX CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;  
 XX Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;  
 XX bactericidal; antibacterial; vaccine; immunostimulatory; infection;  
 XX immune response; ss.

XX Neisseria sp.

XX Key Location/Qualifiers

XX modified\_base 1..22

XX /tag= a  
 XX /note= "preferably contains at least one  
 XX phosphorothioate bond"

XX WO200050075-A2.

XX 31-AUG-2000.

XX 09-FEB-2000; 2000WO-IB00176.

XX 26-FEB-1999; 99US-0121792.

XX (CHIR-) CHIRON SPA.

XX Grandi G, Rapinoli R, Giuliani MM, Pizsa M;

XX WPI; 2001-015529/02.

XX Immunogenic composition useful for stimulating an immune response in a  
 XX mammal against Neisseria infection, comprises Neisseria antigen and an  
 XX adjuvant composition comprising an oligonucleotide with a CG motif -

XX Claim 19; Page 9; 39p; English.

XX The present invention describes an immunogenic composition (I)  
 XX comprising a Neisseria antigen and an adjuvant composition comprising an  
 XX oligonucleotide comprising at least 1 CG motif. Also described is an  
 XX adjuvant composition (II) comprising an oligonucleotide which comprises  
 XX at least 1 CG motif and a complete Freund's adjuvant (CFA), where the  
 XX oligonucleotide preferably comprises at least one phosphorothioate bond.  
 XX AA92359 to AAA92385 represent specifically claimed oligonucleotides of  
 XX the present invention. (I) is useful for stimulating an immune response  
 XX in a mammal, preferably a human, against Neisseria infection, preferably  
 XX Neisseria meningitidis infection, and in the manufacture of a medicament  
 XX for inducing a protective immune response in a mammal.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 22; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
 |||||  
 DB 8 GAACGTCGAGATGA 22

RESULT 38  
 ABV73190  
 ID ABV73190 standard; DNA; 22 BP.



AC ABV73190;  
 XX  
 DT 08-JAN-2003 (first entry)  
 XX  
 XX Nucleotide sequence of an immunostimulatory oligonucleotide ISS-1.  
 DE  
 XX Immunomodulator; immunostimulant; antiinflammatory; antiasthmatic; Th2;  
 KW antiallergic; dermatological; vaccine; gene therapy; immune response; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200274922-A2.  
 XX  
 PD 26-SEP-2002.  
 XX  
 PF 15-MAR-2002; 2002WO-US08207.  
 XX  
 PR 16-MAR-2001; 2001US-276865P.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Broide DH, Raz E;  
 DR WPI; 2002-740857/80.  
 XX  
 PT Suppressing a symptom of an allergic response in a subject, useful for  
 PT preventing inflammation associated with allergy, comprises  
 PT administering to an antigen-sensitized host first and second doses of  
 PT an immunomodulatory nucleic acid -  
 XX  
 PS Examples; Page 27; 98pp; English.  
 XX  
 CC The invention relates to suppressing symptoms of allergic response that  
 CC involves administering to an antigen-sensitized mammalian host a dose of  
 CC a composition comprising an immunomodulatory nucleic acid, and a second  
 CC dose of a composition comprising an immunomodulatory nucleic acid, about  
 CC 1 day - 8 weeks after the first dose. The immunomodulatory nucleic acid  
 CC comprises a nucleotide sequence comprising 5'-GG-3'. The methods are  
 CC useful for suppressing a symptom of an allergic reaction in a subject,  
 CC maintaining suppression of a Th2 immune response and maintaining  
 CC stimulation of a Th1 immune response. One method is useful in preventing  
 CC the onset of, or rapidly suppress, antigen-stimulated inflammation in a  
 CC host. The immunostimulatory nucleic acids are useful in the treatment and  
 CC prevention of inflammation associated with allergy, including antigen-  
 CC stimulated granulocyte infiltration of tissue, such as occurs in the  
 CC respiratory passages of asthmatics during an asthma attack, for boosting  
 CC the immune responsiveness of a mammalian host to a sensitizing antigen,  
 CC and for treating a host suffering from inflammatory conditions such as  
 CC asthma, nasal polypsis, allergic rhinitis, atopic dermatitis, allergic  
 CC conjunctivitis, eosinophilic fasciitis, idiopathic hypereosinophilic  
 CC syndrome, and cutaneous basophil hypersensitivity. The present sequence  
 CC represents the nucleotide sequence of an immunomodulatory  
 CC oligonucleotide.  
 CC  
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 24; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
 |||||  
 DB 8 GAACGTCGAGATGA 22

RESULT 39  
 ID ABQ78627 standard; DNA; 22 BP.  
 XX  
 AC ABQ78627;  
 XX  
 DT 25-NOV-2002 (first entry)  
 XX

DE ISS enhancing HIV-specific Th1 cytokine and humoral responses.  
 XX  
 KW Immunostimulatory sequence; ISS; Th1 cytokine response; humoral response;  
 KW HIV, beta-chemokine; immunisation; AIDS; ss.  
 XX  
 OS unidentified.  
 XX  
 PN WO200258726-A1.  
 XX  
 PD 01-AUG-2002.  
 XX  
 PF 24-JAN-2002; 2002WO-US02077.  
 XX  
 PR 26-JAN-2001; 2001US-264476P.  
 XX  
 PA (IMMU-) IMMUNE RESPONSE CORP.  
 XX  
 PI Moss RB, Carlo DJ;  
 DR WPI; 2002-643331/69.  
 XX  
 PT Treating an HIV-infected individual comprises treatment with  
 PT anti-retroviral compound and immunization with an HIV immunogenic  
 PT composition with structured cycles of anti-retroviral treatment and  
 PT withdrawal from treatment -  
 XX  
 PS Disclosure; Page 15; 31pp; English.  
 XX  
 CC The present sequence represents an exemplary immunostimulatory sequence  
 CC (ISS) which enhances HIV-specific Th1 cytokine and humoral responses,  
 CC and also enhances both non-specific and HIV-specific beta-chemokine  
 CC production. ISSs can be included in HIV immunogenic compositions of  
 CC the invention. The specification describes a method for treating an  
 CC HIV-infected individual, which comprises combining immunisation with an  
 CC anti-retroviral compound, an HIV immunogenic composition with structured  
 CC cycles of anti-retroviral treatment and withdrawal from treatment. The  
 CC advantages of the method of the invention include a delay in the rebound  
 CC to an unacceptably high viral load; a more rapid or sustained increase in  
 CC HIV-specific CD4 T cell counts; a reduction or delay in the development  
 CC of AIDS symptoms, including AIDS-related opportunistic infections; and  
 CC a higher degree of patient compliance with treatment and fewer toxic side  
 CC effects associated with long-term anti-retroviral drug treatment. The  
 CC method is useful for treating an HIV-infected individual.  
 CC  
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 24; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
 |||||  
 DB 8 GAACGTCGAGATGA 22

RESULT 40  
 ID AAL44504 standard; DNA; 22 BP.  
 XX  
 AC AAL44504;  
 XX  
 DT 08-NOV-2002 (first entry)  
 XX  
 DE Cpg motif oligonucleotide #12.  
 XX  
 KW Vaccine; immune response; microparticle; ds; adsorbent surface;  
 KW poly(alpha-hydroxy acid); poly(hydroxy butyric acid); polycaprolactone;  
 KW polyorthoester; polycyanoacrylate; detergent; submicron emulsion;  
 KW viral infection; bacterial infection; parasitic infection;  
 KW Cpg oligonucleotide.  
 XX  
 OS unidentified.  
 XX

```

PN WO200226209-A2.
XX
XX 04-APR-2002.
XX
XX 28-SEP-2001; 2001WO-US30540.
XX
XX 28-SEP-2000; 2000US-236105P.
XX
XX 30-AUG-2001; 2001US-315905P.
XX
XX (CHIR ) CHIRON CORP.
XX
XX O'hagan D, Otten G, Donnelly JJ, Polo JM, Barnett S, Singh M;
XX Ulmer J, Dubensky JW;
XX WPI; 2002-519084/55.
XX
XX A microparticle to which a biologically active macromolecule is
XX adsorbed, for use as a vaccine composition to treat viral, bacterial or
XX parasitic infections, comprises a polymer microparticle, a detergent
XX and a submicron emulsion -
XX
XX PS Disclosure; Page 46; 100pp; English.
XX
XX CC The invention relates to a method of raising an immune response in a host
XX animal. The method of the invention comprises administering a
XX microparticle that has an adsorbent surface to which a first biologically
XX active macromolecule (e.g. a nucleic acid) has been adsorbed. The
XX microparticle comprises a polymer microparticle of poly(alpha-hydroxy
XX acid), a polyhydroxy butyric acid, a polycaprolactone, a polyorthoster,
XX a polyanaoacrylate, a detergent, and submicron emulsion. The method/
XX a polyanaoacrylate, a detergent, and submicron emulsion. The method/
XX against viral, bacterial or parasitic infections. The present DNA
XX sequence represents a Cpg oligonucleotide of the invention.
XX
XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
XX
XX Query Match 71.4%; Score 15; DB 24; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 19;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 GAACGTTGCAGATGA 20
XX |||||
XX 8 GAACGTTGCAGATGA 22
XX
XX Db
XX
XX RESULT 41
XX ID ABQ75153 standard; DNA; 22 BP.
XX
XX AC ABQ75153;
XX
XX DT 05-NOV-2002 (first entry)
XX
XX DE ISS immunomodulatory oligonucleotide SEQ ID NO:2.
XX
XX KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
XX allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
XX idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
XX malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
XX immunoglobulin E; IGE-related disorder; antiallergic; antiasthmatic;
XX virucide; antibacterial; protozoacide; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT misc_RNA 13
XX FT /*tag= a
XX FT /note= "uracil"
XX
XX PN WO200252002-A2.
XX
XX PD 04-JUL-2002.
XX

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PF 27-DEC-2001; 2001WO-US50821.
XX
XX 27-DEC-2000; 2000US-258675P.
XX
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX FI Fearon KL, Dina D;
XX WPI; 2002-657426/70.
XX
XX DR
XX
XX PT Immunomodulatory polynucleotide for modulating an immune response in a
XX subject suffering from disorders associated with Th2-type immune
XX response, e.g. allergy, or infectious disease, comprises an
XX immunostimulatory sequence -
XX
XX PS Claim 4; Page 20; 95pp; English.
XX
XX CC The present invention describes an immunomodulatory polynucleotide (I)
XX comprising an immunostimulatory sequence (ISS). Also described: (1) an
XX immunomodulatory composition comprising (1); (2) an immunomodulatory
XX polynucleotide/microcarrier (IMP/MC) complex, comprising (1) linked to a
XX biodegradable MC, where the MC is less than 10 micrometre in size; and
XX (3) a kit comprising (1). (1) has antiallergic, antiasthmatic, virucide,
XX antibacterial and protozoacide activities, and can be used as a modulator
XX of immune response. (1) is useful for modulating an immune response in an
XX individual suffering from disorders associated with a Th2-type immune
XX response, especially an allergy or asthma, or an infectious disease. (1)
XX is also useful for increasing interferon-gamma (IFN-gamma) in an
XX individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
XX individual having a viral infection. (1) is further useful for
XX ameliorating a symptom of an infectious disease caused by a cellular
XX pathogen such as mycobacterial disease, malaria, leishmaniasis,
XX toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
XX symptom of an immunoglobulin E (IGE)-related disorder, preferably an
XX allergy-related disorder, in particular asthma in an individual. The
XX present sequence represents an immunomodulatory oligonucleotide which
XX is specifically claimed in the present invention.
XX
XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 5 T; 1 U; 0 other;
XX
XX Query Match 71.4%; Score 15; DB 24; Length 22;
XX Best Local Similarity 93.3%; Pred. No. 19;
XX Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 GAACGTTGCAGATGA 20
XX |||||
XX 8 GAACGTTGCAGATGA 22
XX
XX Db
XX
XX RESULT 42
XX ID ABQ75163 standard; DNA; 22 BP.
XX
XX AC ABQ75163;
XX
XX DT 05-NOV-2002 (first entry)
XX
XX DE ISS immunomodulatory oligonucleotide SEQ ID NO:12.
XX
XX KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
XX allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
XX idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
XX malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
XX immunoglobulin E; IGE-related disorder; antiallergic; antiasthmatic;
XX virucide; antibacterial; protozoacide; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT misc_RNA 13
XX FT /*tag= a
XX FT /note= "uracil"
XX
XX PN WO200252002-A2.
XX
XX PD 04-JUL-2002.
XX
XX PF 27-DEC-2001; 2001WO-US50821.
XX

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XX 27-DEC-2000; 2000US-258675P.
XX
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX Fearon KL, Dina D;
XX
XX WPI; 2002-657426/70.
XX
XX Immunomodulatory polynucleotide for modulating an immune response in a
XX subject suffering from disorders associated with Th2-type immune
XX response, e.g. allergy, or infectious disease, comprises an
XX immunostimulatory sequence
XX
XX Example 1; Page 20; 95pp; English.
XX
XX The present invention describes an immunomodulatory polynucleotide (I)
XX comprising an immunostimulatory sequence (ISS). Also described: (1) an
XX immunomodulatory composition comprising (1); (2) an immunomodulatory
XX polynucleotide/microcarrier (IMP/MC) complex, comprising (1) linked to a
XX biodegradable MC, where the MC is less than 10 micrometre in size; and
XX (3) a kit comprising (1). (1) has anti-allergic, antiasthmatic, virucide,
XX antibacterial and protozoacide activities, and can be used as a modulator
XX of immune response. (1) is useful for modulating an immune response in an
XX individual suffering from disorders associated with a Th2-type immune
XX response, especially an allergy or asthma, or an infectious disease. (1)
XX is also useful for increasing interferon-gamma (IFN-gamma) in an
XX individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
XX individual having a viral infection. (1) is further useful for
XX ameliorating a symptom of an infectious disease caused by a cellular
XX pathogen such as mycobacterial disease, malaria, leishmaniasis,
XX toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
XX symptom of an immunoglobulin E (IgE)-related disorder, preferably an
XX allergy-related disorder, in particular asthma in an individual. The
XX present sequence represents an immunomodulatory oligonucleotide from
XX the present invention.
XX
XX Sequence 22 BP; 5 A; 4 C; 7 G; 6 T; 0 other;
XX
XX Query Match 71.4%; Score 15; DB 24; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 19;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Oy 6 GAAGCTTCGAGATGA 20
XX |||||
XX Db 8 GAAGCTTCGAGATGA 22
XX
XX RESULT 43
XX ABQ75173
XX ID ABQ75173 standard; DNA; 22 BP.
XX
XX AC ABQ75173;
XX
XX DT 05-NOV-2002 (first entry)
XX
XX DE ISS immunomodulatory oligonucleotide SEQ ID NO:22.
XX
XX Immunostimulatory sequence; ISS: immunomodulatory; immune response;
XX allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
XX idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
XX malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
XX immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
XX virucide; antibacterial; protozoacide; ss.
XX
XX Synthetic.
XX
XX WO200252002-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-US50821.
XX

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PR 27-DEC-2000; 2000US-258675P.
XX
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX Fearon KL, Dina D;
XX
XX WPI; 2002-657426/70.
XX
XX Immunomodulatory polynucleotide for modulating an immune response in a
XX subject suffering from disorders associated with Th2-type immune
XX response, e.g. allergy, or infectious disease, comprises an
XX immunostimulatory sequence
XX
XX Example 1; Page 20; 95pp; English.
XX
XX The present invention describes an immunomodulatory polynucleotide (I)
XX comprising an immunostimulatory sequence (ISS). Also described: (1) an
XX immunomodulatory composition comprising (1); (2) an immunomodulatory
XX polynucleotide/microcarrier (IMP/MC) complex, comprising (1) linked to a
XX biodegradable MC, where the MC is less than 10 micrometre in size; and
XX (3) a kit comprising (1). (1) has anti-allergic, antiasthmatic, virucide,
XX antibacterial and protozoacide activities, and can be used as a modulator
XX of immune response. (1) is useful for modulating an immune response in an
XX individual suffering from disorders associated with a Th2-type immune
XX response, especially an allergy or asthma, or an infectious disease. (1)
XX is also useful for increasing interferon-gamma (IFN-gamma) in an
XX individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
XX individual having a viral infection. (1) is further useful for
XX ameliorating a symptom of an infectious disease caused by a cellular
XX pathogen such as mycobacterial disease, malaria, leishmaniasis,
XX toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
XX symptom of an immunoglobulin E (IgE)-related disorder, preferably an
XX allergy-related disorder, in particular asthma in an individual. The
XX present sequence represents an immunomodulatory oligonucleotide from
XX the present invention.
XX
XX Sequence 22 BP; 4 A; 6 C; 6 G; 6 T; 0 other;
XX
XX Query Match 71.4%; Score 15; DB 24; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 19;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Oy 1 TCGTGAACGTTGCA 15
XX |||||
XX Db 1 TCGTGAACGTTGCA 15
XX
XX RESULT 44
XX ABQ75206
XX ID ABQ75206 standard; DNA; 22 BP.
XX
XX AC ABQ75206;
XX
XX DT 05-NOV-2002 (first entry)
XX
XX DE ISS immunomodulatory oligonucleotide SEQ ID NO:40.
XX
XX Immunostimulatory sequence; ISS: immunomodulatory; immune response;
XX allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
XX idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
XX malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
XX immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
XX virucide; antibacterial; protozoacide; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT misc_RNA 14
XX FT /*tag= a
XX FT /note= "uracil"
XX
XX WO200252002-A2.
XX

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PD 04-JUL-2002.  
 XX 27-DEC-2001; 2001WO-US50821.  
 PF 27-DEC-2001; 2000US-258675P.  
 XX 27-DEC-2000; 2000US-258675P.  
 PR  
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 PA  
 XX Fearon KL, Dina D;  
 PI  
 XX WPI; 2002-657426/70.  
 DR  
 XX Immunomodulatory polynucleotide for modulating an immune response in a  
 PT subject suffering from disorders associated with Th2-type immune  
 PT response, e.g. allergy, or infectious disease, comprises an  
 PT immunostimulatory sequence -  
 PS  
 XX Disclosure; Page 22; 95pp; English.  
 CC The present invention describes an immunomodulatory polynucleotide (1)  
 CC comprising an immunostimulatory sequence (ISS). Also described: (1) an  
 CC immunomodulatory composition comprising (1); (2) an immunomodulatory  
 CC polynucleotide/microcarrier (IMP/MC) complex, comprising (1) linked to a  
 CC biodegradable MC, where the MC is less than 10 micrometre in size; and  
 CC (3) a kit comprising (1). (1) has anti-allergic, antiasthmatic, virucide,  
 CC antibacterial and protozoacide activities, and can be used as a modulator  
 CC of immune response. (1) is useful for modulating an immune response in an  
 CC individual suffering from disorders associated with a Th2-type immune  
 CC response, especially an allergy or asthma, or an infectious disease. (1)  
 CC is also useful for increasing interferon-gamma (IFN-gamma) in an  
 CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an  
 CC individual having a viral infection. (1) is further useful for  
 CC ameliorating a symptom of an infectious disease caused by a cellular  
 CC pathogen such as mycobacterial disease, malaria, leishmaniasis,  
 CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a  
 CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an  
 CC allergy-related disorder, in particular asthma in an individual. The  
 CC present sequence represents an immunomodulatory oligonucleotide from  
 CC the present invention.  
 CC  
 XX Sequence 22 BP; 6 A; 3 C; 7 G; 5 T; 1 U; 0 other;  
 SQ  
 Query Match 71.4%; Score 15; DB 24; Length 22;  
 Best Local Similarity 93.3%; Pred. No. 19;  
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GAACGTTGAGATGA 20  
 Db 8 GAACGTTGAGATGA 22  
 RESULT 45  
 ABQ75211  
 ID ABQ75211 standard; DNA; 22 BP.  
 AC  
 XX ABQ75211;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE ISS immunomodulatory oligonucleotide SEQ ID NO:45.  
 XX  
 KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;  
 KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;  
 KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;  
 KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;  
 KW immunoglobulin E; IgE-related disorder; anti-allergic; antiasthmatic;  
 KW virucide; antibacterial; protozoacide; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 2 /\*tag= a  
 FT

FT /mod\_base= OTHER  
 FT /note= "5-bromocytosine"  
 FT modified\_base 5  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "5-bromocytosine"  
 FT  
 PN WO200252002-A2.  
 XX  
 PD 04-JUL-2002.  
 XX  
 XX 27-DEC-2001; 2001WO-US50821.  
 PF 27-DEC-2001; 2000US-258675P.  
 PR 27-DEC-2000; 2000US-258675P.  
 XX  
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 PA  
 XX Fearon KL, Dina D;  
 PI  
 XX WPI; 2002-657426/70.  
 DR  
 XX Immunomodulatory polynucleotide for modulating an immune response in a  
 PT subject suffering from disorders associated with Th2-type immune  
 PT response, e.g. allergy, or infectious disease, comprises an  
 PT immunostimulatory sequence -  
 PS  
 XX Example 1; Page 22; 95pp; English.  
 CC The present invention describes an immunomodulatory polynucleotide (1)  
 CC comprising an immunostimulatory sequence (ISS). Also described: (1) an  
 CC immunomodulatory composition comprising (1); (2) an immunomodulatory  
 CC polynucleotide/microcarrier (IMP/MC) complex, comprising (1) linked to a  
 CC biodegradable MC, where the MC is less than 10 micrometre in size; and  
 CC (3) a kit comprising (1). (1) has anti-allergic, antiasthmatic, virucide,  
 CC antibacterial and protozoacide activities, and can be used as a modulator  
 CC of immune response. (1) is useful for modulating an immune response in an  
 CC individual suffering from disorders associated with a Th2-type immune  
 CC response, especially an allergy or asthma, or an infectious disease. (1)  
 CC is also useful for increasing interferon-gamma (IFN-gamma) in an  
 CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an  
 CC individual having a viral infection. (1) is further useful for  
 CC ameliorating a symptom of an infectious disease caused by a cellular  
 CC pathogen such as mycobacterial disease, malaria, leishmaniasis,  
 CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a  
 CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an  
 CC allergy-related disorder, in particular asthma in an individual. The  
 CC present sequence represents an immunomodulatory oligonucleotide from  
 CC the present invention.  
 CC  
 XX Sequence 22 BP; 5 A; 2 C; 7 G; 6 T; 2 other;  
 SQ  
 Query Match 71.4%; Score 15; DB 24; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GAACGTTGAGATGA 20  
 Db 8 GAACGTTGAGATGA 22  
 RESULT 46  
 ABQ75212  
 ID ABQ75212 standard; DNA; 22 BP.  
 AC  
 XX ABQ75212;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE ISS immunomodulatory oligonucleotide SEQ ID NO:46.  
 XX  
 KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;  
 KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;  
 KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;  
 KW

KV	malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW	immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KM	viricide; antibacterial; protozoacide; ss.
XX	
OS	Synthetic.
XX	
PH	Key
FT	modified_base
FT	5
FT	/*tag= a
FT	/mod_base= OTHER
FT	/note= "5-Bromocytosine"
XX	
PN	MO200252002-A2.
XX	
PD	04-JUL-2002.
XX	
PF	27-DEC-2001; 2001WO-US50821.
XX	
PR	27-DEC-2000; 2000US-258675P.
XX	
PA	(DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX	
PI	Fearon KL, Dina D;
XX	
DR	WPI, 2002-657426/70.
XX	
PT	Immunomodulatory polynucleotide for modulating an immune response in a
PT	subject suffering from disorders associated with Th2-type immune
PT	response, e.g. allergy, or infectious disease, comprises an
PT	immunostimulatory sequence
XX	
PS	Example 1, Page 22; 95pp; English.
XX	
CC	The present invention describes an immunomodulatory polynucleotide (I)
CC	comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC	immunomodulatory composition comprising (I); (2) an immunomodulatory
CC	polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC	biodegradable MC, where the MC is less than 10 micrometre in size; and
CC	(3) a kit comprising (I). (I) has: antiallergic, antiasthmatic, virucide,
CC	antibacterial and protozoacide activities, and can be used as a modulator
CC	of immune response. (I) is useful for modulating an immune response in an
CC	individual suffering from disorders associated with a Th2-type immune
CC	response, especially an allergy or asthma, or an infectious disease. (I)
CC	is also useful for increasing interferon-gamma (IFN-gamma) in an
CC	individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC	individual having a viral infection. (I) is further useful for
CC	ameliorating a symptom of an infectious disease caused by a cellular
CC	pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC	toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC	symptom of an immunoglobulin B (IgB)-related disorder, preferably an
CC	allergy-related disorder, in particular asthma in an individual. The
CC	present sequence represents an immunomodulatory oligonucleotide from
CC	the present invention.
XX	
SQ	Sequence 22 BP; 5 A; 3 C; 7 G; 6 T; 1 other;
XX	
QY	Query Match 71.4%; Score 15; DB 24; Length 22;
XX	Best Local Similarity 100.0%; Pred. No. 19;
DB	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	
6	GAACGTTGCAGATGA 20
8	GAACGTTGCAGATGA 22
XX	
RESULT 47	
ABQ75259	
ID	ABQ75259 standard; DNA; 22 BP.
XX	
AC	ABQ75259;
XX	
DT	05-NOV-2002 (first entry)
XX	

[illegible]

XX Cell death; DNA damage; DNA-dependent protein kinase; DNA-PK; necrosis;  
 KW immune response; apoptosis; Alzheimer's disease; Parkinson's disease;  
 KW rheumatoid arthritis; inflammation; osteoporosis; myocardial infarction;  
 KW liver disease; reperfusion injury; carcinoma; multiple sclerosis; stroke;  
 KW amyotrophic lateral sclerosis; Acquired Immune Deficiency Syndrome; AIDS;  
 KW head injury damage; aplastic anaemia; tumour; organ transplantation;  
 KW cerebral infarction; follicular lymphomas; systemic lupus erythematosus;  
 KW viral infection; glomerulonephritis; apoptosis; autoimmune disorder;  
 KW sepsis; immunostimulatory oligodeoxynucleotide; ISS-ODN; ss.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200185910-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 04-MAY-2001; 2001WO-US14508.  
 XX  
 PR 05-MAY-2000; 2000US-202274P.  
 XX  
 PR 17-JAN-2001; 2001US-262321P.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Raz E, Lois AF, Takabayashi K;  
 XX  
 DR WPI, 2002-062244/08.  
 XX  
 PT Modulating cell death or reducing DNA damage in eukaryotic cells,  
 PT useful for reducing cell death in individual or organ, comprises  
 PT contacting cell with agent modulating biological activity of  
 PT DNA-dependent protein kinase -  
 XX  
 PS Example 1; Page 29; 57pp; English.  
 XX  
 CC The invention relates to a method for modulating cell death or reducing  
 CC DNA damage in an eukaryotic cell by contacting the cell with an agent  
 CC that modulates the biological activity of DNA-dependent protein kinase  
 CC (DNA-PK). The invention also relates nucleic acids which modulate the  
 CC immune response binding to Ku antigen, resulting in activation of DNA-PK.  
 CC The method is useful for modulating cell death or reducing DNA damage in  
 CC an eukaryotic cell, for treating any disorder resulting from a genotoxic  
 CC agent to a cell e.g., necrosis, apoptosis. The method is also useful  
 CC for treating cell death-related indications such as Alzheimer's disease,  
 CC Parkinson's disease, rheumatoid arthritis, septic shock, sepsis, stroke,  
 CC central nervous system inflammation, osteoporosis, degenerative liver  
 CC disease, cerebellar degeneration, reperfusion injury, multiple sclerosis,  
 CC amyotrophic lateral sclerosis, myocardial infarction, head injury damage,  
 CC acquired immunodeficiency syndrome (AIDS), aplastic anaemia, cerebral  
 CC infarction, bypass heart surgery, organ transplantation. The method is  
 CC also useful for treating follicular lymphomas, carcinomas, autoimmune  
 CC disorders (systemic lupus erythematosus), hormone dependent tumours,  
 CC immune mediated glomerulonephritis; apoptosis and viral infections. The  
 CC present sequence is immunostimulatory oligodeoxynucleotide (ISS-ODN)  
 CC used for identifying ISS-binding protein, which is used in the  
 CC exemplification of the invention.  
 CC  
 XX  
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;  
 QY  
 Query Match 71.4%; Score 15; DB 24; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 8 GAACGTCGAGATGA 20  
 6 GAACGTCGAGATGA 20  
 8 GAACGTCGAGATGA 22

RESULT 49  
 AAS16337  
 ID AAS16337 standard; DNA; 22 BP.  
 XX  
 AC AAS16337;

XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE ISS polynucleotide #1 useful for treating herpes virus infections.  
 XX  
 KW Herpes simplex virus; HSV infection; immunostimulatory sequence; ISS;  
 KW immune response; alphaherpesvirinae; herpes virus zoster virus; VZV;  
 KW HSV-1; HSV-2; chicken pox; herpes labialis; cold sore; genital herpes;  
 KW virucide; phosphorothioate; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..22  
 FT /tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Optionally phosphorothioate internucleotide  
 FT linkages"  
 XX  
 PN WO200168103-A2.  
 XX  
 PD 20-SEP-2001.  
 XX  
 PF 12-MAR-2001; 2001WO-US07841.  
 XX  
 PR 10-MAR-2000; 2000US-188556P.  
 XX  
 PR 09-MAR-2001; 2001US-0802518.  
 XX  
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 XX  
 PI Van Nest G;  
 XX  
 DR WPI, 2002-041171/05.  
 XX  
 PT Preventing, reducing the severity or reducing the recurrence of an  
 PT infection or symptom of herpes simplex virus (HSV), e.g. HSV-2,  
 PT comprises administering an immunostimulatory sequence to an individual  
 PT -  
 XX  
 PS Claim 5; Page 41; 49pp; English.  
 XX  
 CC The present invention relates to novel methods of treating, preventing,  
 CC or reducing the severity or recurrence of a symptom of herpes simplex  
 CC virus (HSV) infection in an individual who has been exposed to or who is  
 CC infected with HSV. The method comprises administering a polynucleotide  
 CC having an immunostimulatory sequence (ISS; AAS16337-AAS16345) which  
 CC induces an immune response. A composition containing ISS is administered  
 CC without a HSV (alphaherpesvirinae) antigen. The composition can be  
 CC included in a kit for ameliorating or preventing a symptom of HSV  
 CC infection caused by herpes virus zoster virus (VZV), HSV-1 and  
 CC particularly HSV-2. Such HSV infections include chicken pox, herpes  
 CC labialis (cold sores) and genital herpes. The present sequence represents  
 CC one of the ISS polynucleotides of the invention.  
 CC Note: The present sequence is shown as single stranded in the  
 CC specification, but the patentees state on page 20 that this sequence may  
 CC be double stranded.  
 CC  
 XX  
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;  
 QY  
 Query Match 71.4%; Score 15; DB 24; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 8 GAACGTCGAGATGA 20  
 6 GAACGTCGAGATGA 20  
 8 GAACGTCGAGATGA 22

RESULT 50  
 AAS16338  
 ID AAS16338 standard; DNA; 22 BP.  
 XX  
 AC AAS16338;

XX 14-FEB-2002 (first entry)  
 DT  
 XX  
 DE ISS polynucleotide #2 useful for treating herpes virus infections.  
 XX  
 KW Herpes simplex virus; HSV infection; immunostimulatory sequence; ISS;  
 KW immune response; alphaherpesvirinae; herpes virus zoster virus; VZV;  
 KW HSV-1; HSV-2; chicken pox; herpes labialis; cold sore; genital herpes;  
 KW virucide; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200168103-A2.  
 XX  
 PD 20-SEP-2001.  
 XX  
 PF 12-MAR-2001; 2001WO-US07841.  
 XX  
 PR 10-MAR-2000; 2000US-188556P.  
 XX  
 PR 09-MAR-2001; 2001US-0802518.  
 XX  
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 XX  
 PI Van Nest G;  
 XX  
 DR WPI; 2002-041171/05.  
 XX  
 PT Preventing, reducing the severity or reducing the recurrence of an  
 PT infection or symptom of herpes simplex virus (HSV), e.g. HSV-2,  
 PT comprises administering an immunostimulatory sequence to an individual  
 PT  
 XX  
 PS Disclosure; Page 19; 49pp; English.  
 XX  
 CC The present invention relates to novel methods of treating, preventing,  
 CC or reducing the severity or recurrence of a symptom of herpes simplex  
 CC virus (HSV) infection in an individual who has been exposed to or who is  
 CC infected with HSV. The method comprises administering a polynucleotide  
 CC having an immunostimulatory sequence (ISS; AAS16337-AAS16345) which  
 CC induces an immune response. A composition containing ISS is administered  
 CC without a HSV (alphaherpesvirinae) antigen. The composition can be  
 CC included in a kit for ameliorating or preventing a symptom of HSV  
 CC infection caused by herpes virus zoster virus (VZV), HSV-1 and  
 CC particularly HSV-2. Such HSV infections include chicken pox, herpes  
 CC labialis (cold sore) and genital herpes. The present sequence represents  
 CC one of the ISS polynucleotides of the invention.  
 CC Note: The present sequence is shown as single stranded in the  
 CC specification, but the patentees state on page 20 that this sequence may  
 CC be double stranded.  
 CC  
 SO Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;  
 SQ  
 Query Match 71.4%; Score 15; DB 24; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GAACGTTGAGATGA 20  
 |||||  
 DB 8 GAACGTTGAGATGA 22  
 |||||  
 RESULT 51  
 AAS16348  
 ID AAS16348 standard; DNA; 22 BP.  
 XX  
 AC AAS16348;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE ISS polynucleotide #1 useful for treating papillomavirus infections.  
 XX  
 KW Animal papillomavirus infection; human papillomavirus; HPV; STD; wart;  
 KW sexually transmitted disease; cervical cancer; immune response;  
 KW

KW immunostimulatory sequence; ISS; virucide; phosphorothioate; ss.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..22  
 FT /tag= a  
 FT /mod base= OTHER  
 FT /note= "Optionally phosphorothioate linkages"  
 XX  
 PN WO200168117-A2.  
 XX  
 PD 20-SEP-2001.  
 XX  
 PF 12-MAR-2001; 2001WO-US07842.  
 XX  
 PR 10-MAR-2000; 2000US-188265P.  
 XX  
 PR 09-MAR-2001; 2001US-0802445.  
 XX  
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 XX  
 PI Van Nest G;  
 XX  
 DR WPI; 2002-041172/05.  
 XX  
 PT Treating, preventing or ameliorating papillomavirus infections,  
 PT comprises administering a composition comprising a polynucleotide  
 PT having an immunostimulatory sequence to the individual  
 PT  
 XX  
 PS Claim 4; Page 39; 44pp; English.  
 XX  
 CC The present invention relates to novel methods of treating, preventing,  
 CC or reducing the severity or recurrence of a symptom of papillomavirus  
 CC infection in an individual that has been exposed to or who is infected  
 CC with papillomavirus. The method comprises administering a polynucleotide  
 CC having an immunostimulatory sequence (ISS; AAS16348-AAS16355) which  
 CC induces an immune response. A composition containing ISS is administered  
 CC without a papillomavirus antigen. The composition can be included in a  
 CC kit for ameliorating or preventing a symptom of human or animal  
 CC papillomavirus infection. Infections with human papillomavirus (HPV)  
 CC which can be prevented or treated using the method of the invention  
 CC include sexually transmitted diseases (STDs), warts, papillomas and  
 CC cervical cancer. The present sequence represents one of the ISS  
 CC polynucleotides of the invention.  
 CC Note: The present sequence is shown as single stranded in the  
 CC specification, but the patentees state on page 20 that this sequence may  
 CC be double stranded.  
 CC  
 SO Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;  
 SQ  
 Query Match 71.4%; Score 15; DB 24; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 GAACGTTGAGATGA 20  
 |||||  
 DB 8 GAACGTTGAGATGA 22  
 |||||  
 RESULT 52  
 AAS16349  
 ID AAS16349 standard; DNA; 22 BP.  
 XX  
 AC AAS16349;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE ISS polynucleotide #2 useful for treating papillomavirus infections.  
 XX  
 KW Animal papillomavirus infection; human papillomavirus; HPV; STD; wart;  
 KW sexually transmitted disease; cervical cancer; immune response;  
 KW immunostimulatory sequence; ISS; virucide; ss.  
 KW



OS Synthetic.  
 XX WO200168117-A2.  
 PN 20-SEP-2001.  
 XX 12-MAR-2001; 2001WO-US07842.  
 XX 10-MAR-2000; 2000US-188265P.  
 PR 09-MAR-2001; 2001US-0802445.  
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 PA Van Nest G;  
 PI Van Nest G;  
 DR WPI; 2002-041172/05.  
 XX  
 XX Treating, preventing or ameliorating papillomavirus infections,  
 PT comprising administering a composition comprising a polynucleotide  
 PT having an immunostimulatory sequence to the individual  
 XX  
 XX Disclosure; Page 19; 44pp; English.  
 XX  
 XX The present invention relates to novel methods of treating, preventing,  
 CC or reducing the severity or recurrence of a symptom of papillomavirus  
 CC infection in an individual that has been exposed to or who is infected  
 CC with papillomavirus. The method comprises administering a polynucleotide  
 CC having an immunostimulatory sequence (ISS; AAS16348-AAS16355) which  
 CC induces an immune response. A composition containing ISS is administered  
 CC without a papillomavirus antigen. The composition can be included in a  
 CC kit for ameliorating or preventing a symptom of human or animal  
 CC papillomavirus infection. Infections with human papillomavirus (HPV)  
 CC which can be prevented or treated using the method of the invention  
 CC include sexually transmitted diseases (STDs), warts, papillomas and  
 CC cervical cancer. The present sequence represents one of the ISS  
 CC polynucleotides of the invention.  
 CC Note: The present sequence is shown as single stranded in the  
 CC specification, but the patentees state on page 20 that this sequence may  
 CC be double stranded.  
 CC  
 XX Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;  
 SQ  
 Query Match 71.4%; Score 15; DB 24; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 6 GAACGTCGAGATGA 20  
 Db 8 GAACGTCGAGATGA 22  
 RESULT 53  
 AAD21877  
 ID AAD21877 standard; DNA; 22 BP.  
 AC AAD21877;  
 XX  
 DT 12-FEB-2002 (first entry)  
 XX  
 DE Immunostimulatory sequence oligonucleotide (ISS-ODN) #1.  
 XX  
 XX Cytotoxic T lymphocyte; CTL; T cell; tumour load; cancer radiotherapy;  
 KW immunostimulatory sequence oligonucleotide; ISS-ODN; chemotherapy;  
 KW immunosuppression; transplantation; autoimmune disease; infection;  
 KW acquired immune deficiency syndrome; AIDS; intracellular pathogen;  
 KW cytomegalovirus; mycobacterial infection; Epstein-Barr virus;  
 KW varicella zoster virus; human immunodeficiency virus; HIV;  
 KW phosphorothioate backbone; ss.  
 XX  
 OS Unidentified.  
 XX  
 XX Key Location/Qualifiers  
 FT modified\_base 1..22

FT /\*tag= a  
 FT /mod\_base= OTHER  
 FT /note= "Phosphorothioate backbone"  
 FT modified\_base 1  
 FT /\*tag= b  
 FT /mod\_base= OTHER  
 FT /note= "Disulphide thymine"  
 XX  
 XX WO200172123-A1.  
 XX 04-OCT-2001.  
 XX 28-MAR-2001; 2001WO-US10118.  
 XX 28-MAR-2000; 2000US-192537P.  
 PR 11-MAY-2000; 2000US-203567P.  
 PR 05-JUL-2000; 2000US-215895P.  
 XX (RSCC) UNIV CALIFORNIA.  
 PA (VETE-) DEPT VETERANS AFFAIRS.  
 XX  
 XX Raz E, Cho HJ, Richman DD, Horner AA;  
 PI WPI; 2002-010699/01.  
 XX  
 XX Increasing antigen-specific cytotoxic T lymphocyte activity in a CD4+ T  
 PT cell deficient individual, useful to treat immunodeficiency and block  
 PT HIV infection, comprises administering immunostimulatory nucleic acid  
 PT -  
 XX  
 XX Example 1; Page 44; 91pp; English.  
 XX  
 XX The present invention relates to a method for increasing antigen-specific  
 CC cytotoxic T lymphocyte (CTL) activity in a CD4+ T cell-deficient  
 CC individual, comprising administering an immunostimulatory sequence  
 CC oligonucleotide (ISS-ODN). The immunostimulatory nucleic acids of the  
 CC invention are used in CD4+ T cell-deficient individuals to decrease  
 CC tumour load, to treat a primary or acquired immunodeficiency,  
 CC particularly where the acquired immunodeficiency is temporary and due  
 CC to cancer radiotherapy or chemotherapy or immunosuppression following  
 CC bone marrow or organ transplantation, or autoimmune disease treatment,  
 CC or is acquired immunodeficiency syndrome (AIDS). The nucleic acids may  
 CC be used to treat a person at risk of becoming CD4+ T cell-deficient,  
 CC particularly where someone at risk of cancer recurrence. They are also  
 CC used to treat infection, particularly by an intracellular pathogen,  
 CC especially one caused by cytomegalovirus, Mycobacterium tuberculosis,  
 CC M. avium, Epstein-Barr virus, a fungus yeast, varicella zoster virus or  
 CC human immunodeficiency virus (HIV). The present sequence is a 5'  
 CC dinucleotide-linked phosphorothioate immunostimulatory sequence  
 CC oligonucleotide (ISS-ODN), used in the exemplification of the invention.  
 CC  
 XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;  
 SQ  
 Query Match 71.4%; Score 15; DB 24; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 6 GAACGTCGAGATGA 20  
 Db 8 GAACGTCGAGATGA 22  
 RESULT 54  
 ABA03833  
 ID ABA03833 standard; DNA; 22 BP.  
 AC ABA03833;  
 XX  
 DT 12-FEB-2002 (first entry)  
 XX  
 DE Immunostimulatory sequence (ISS) SEQ ID NO:1.  
 XX  
 XX Immunomodulatory polynucleotide/microcarrier complex; IMP/MC; IGB;  
 KW





Db 8 GAACGTCGAGATGA 22

## RESULT 56

ABA03844  
ID ABA03844 standard; DNA; 22 BP.

XX ABA03844;

DT 12-FEB-2002 (first entry)

XX Immunostimulatory sequence (ISS) SEQ ID NO:1.

XX Immunostimulatory sequence; ISS; immunostimulation; viral infection;  
KW immunomodulation; virucide; gene therapy; viraemia; phosphorothioate; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT modified\_base 1..22

FT /tag= a

FT /mod\_base= OTHER

FT /note= "phosphorothioate linkages"

XX WO200168077-A2.

XX 20-SEP-2001.

XX 12-MAR-2001; 2001WO-US07840.

XX 10-MAR-2000; 2000US-188302P.

XX 09-MAR-2001; 2001US-0802685.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Van Nest G;

XX WPI; 2002-048999/06.

XX Reducing severity, recurrence or duration of symptom of virus

XX infection, or reducing viraemia or blood levels of virus antigen,

XX comprises administering a polynucleotide having an immunostimulatory

XX sequence -

XX Claim 4; Page 54; 65pp; English.

XX The present invention describes a method for reducing severity of a

XX symptom of virus infection in an individual infected with a virus. The

XX method comprises administering a composition consisting of a

XX polynucleotide having an immunostimulatory sequence (ISS). The ISS

XX comprises the sequence 5'-C-G-pyrimidine,pyrimidine,C-G-3'. An antigen

XX is administered in conjunction with the composition. ISS has virucide

XX activity and can be used in gene therapy. The method using the ISS can

XX be used for suppressing, ameliorating and/or preventing viral infections

XX to an individual who may be at risk of being exposed to, exposed to or

XX infected by a virus. It may also be used in reducing the recurrence

XX or duration of a symptom of viral infection, delaying the development

XX of a virus infection, and reducing viraemia or blood levels of virus

XX antigens. The present sequence represents a specifically claimed ISS

XX for use in the method of the invention.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

XX Query Match 71.4%; Score 15; DB 24; Length 22;

XX Best Local Similarity 100.0%; Pred. No. 19;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 6 GAACGTCGAGATGA 20

XX 8 GAACGTCGAGATGA 22

RESULT 57  
ABA03845  
ID ABA03845 standard; DNA; 22 BP.

XX ABA03845;

DT 12-FEB-2002 (first entry)

XX Immunostimulatory sequence (ISS) SEQ ID NO:2.

XX Immunostimulatory sequence; ISS; immunostimulation; viral infection;

XX immunomodulation; virucide; gene therapy; viraemia; ss.

XX Synthetic.

XX WO200168077-A2.

XX 20-SEP-2001.

XX 12-MAR-2001; 2001WO-US07840.

XX 10-MAR-2000; 2000US-188302P.

XX 09-MAR-2001; 2001US-0802685.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Van Nest G;

XX WPI; 2002-048999/06.

XX Reducing severity, recurrence or duration of symptom of virus

XX infection, or reducing viraemia or blood levels of virus antigen,

XX comprises administering a polynucleotide having an immunostimulatory

XX sequence -

XX Disclosure; Page 20; 65pp; English.

XX The present invention describes a method for reducing severity of a

XX symptom of virus infection in an individual infected with a virus. The

XX method comprises administering a composition consisting of a

XX polynucleotide having an immunostimulatory sequence (ISS). The ISS

XX comprises the sequence 5'-C-G-pyrimidine,pyrimidine,C-G-3'. An antigen

XX is administered in conjunction with the composition. ISS has virucide

XX activity and can be used in gene therapy. The method using the ISS can

XX be used for suppressing, ameliorating and/or preventing viral infections

XX to an individual who may be at risk of being exposed to, exposed to or

XX infected by a virus. It may also be used in reducing the recurrence

XX or duration of a symptom of viral infection, delaying the development

XX of a virus infection, and reducing viraemia or blood levels of virus

XX antigens. The present sequence represents an ISS given in the

XX exemplification of the present invention.

XX Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;

XX Query Match 71.4%; Score 15; DB 24; Length 22;

XX Best Local Similarity 100.0%; Pred. No. 19;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 6 GAACGTCGAGATGA 20

XX 8 GAACGTCGAGATGA 22

## RESULT 58

ABA03856  
ID ABA03856 standard; DNA; 22 BP.

XX ABA03856;

DT 12-FEB-2002 (first entry)

XX Immunostimulatory sequence (ISS) SEQ ID NO:1.

XX Immunostimulatory sequence; ISS; immunomodulation; HBV; HCV; infection;  
KW hepatitis B virus; hepatitis C virus; virucide; anti-inflammatory;  
KW hepatotropic; gene therapy; hepatitis infection; viraemia; jaundice;  
KW fatigue; abdominal pain; portal hypertension; cirrhosis;  
KM phosphorochioate; ss.  
XX  
XX Synthetic.  
OS  
FH Key location/Qualifiers  
FT modified\_base 1..22  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "phosphorochioate linkages"  
XX  
XX WO200168078-A2.  
XX  
XX 20-SEP-2001.  
XX  
XX 12-MAR-2001; 2001WO-US07931.  
XX  
XX 10-MAR-2000; 2000US-188301P.  
PR 09-MAR-2001; 2001US-0802370.  
XX  
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
XX  
XX Van Nest G;  
XX  
XX WPI; 2002-049000/06.  
XX  
XX Reducing viremia and blood levels of hepatitis virus antigen in an  
PT individual infected with hepatitis B virus, comprises administering a  
PT composition comprising a polynucleotide having an immunostimulatory  
PT sequence -  
XX  
XX Claim 5; Page 38; 43pp; English.  
XX  
XX The present invention describes a method for reducing viraemia or blood  
CC levels of a hepatitis virus antigen in an individual infected with  
CC hepatitis B virus (HBV). The method comprises administering a composition  
CC comprising a polynucleotide having an immunostimulatory sequence (ISS)  
CC to the individual, where the ISS comprises the sequence 5'-C, G-3', an  
CC HBV antigen is not administered in conjunction with administration of  
CC the composition, and where the composition is administered in an amount  
CC sufficient to reduce HBV viraemia or blood levels of a hepatitis virus  
CC antigen. ISS has virucide, anti-inflammatory and hepatotropic activities,  
CC and can be used in gene therapy. The method can be used for suppressing  
CC and/or ameliorating hepatitis infection in an individual, especially for  
CC preventing, palliating, ameliorating, reducing and/or eliminating one or  
CC more symptoms of HBV or HCV (hepatitis C virus) infection without  
CC administering HBV or HCV antigens. The method is specifically useful for  
CC reducing viraemia and hepatitis viral antigen in blood. ISS-containing  
CC polynucleotides may also be used to improve physical symptoms such as  
CC jaundice, fatigue, abdominal pain, and other clinical/laboratory  
CC findings associated with hepatitis such as blood levels of liver enzymes,  
CC portal hypertension, or cirrhosis. The present sequence represents a  
CC specifically claimed ISS oligonucleotide for use in the method of the  
CC invention.  
XX  
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;  
SQ  
Query Match 71.4%; Score 15; DB 24; Length 22;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20  
|||  
Db 8 GAACGTTGAGATGA 22

RESULT 59  
ABA03857 standard; DNA; 22 BP.  
XX

AC ABA03857;  
XX  
XX 12-FEB-2002 (first entry)  
XX  
XX Immunostimulatory sequence (ISS) SEQ ID NO:2.  
DE  
XX  
XX Immunostimulatory sequence; ISS; immunomodulation; HBV; HCV; infection;  
KW hepatitis B virus; hepatitis C virus; virucide; anti-inflammatory;  
KW hepatotropic; gene therapy; hepatitis infection; viraemia; jaundice;  
KW fatigue; abdominal pain; portal hypertension; cirrhosis; ss.  
XX  
XX Synthetic.  
OS  
XX  
XX WO200168078-A2.  
XX  
XX 20-SEP-2001.  
XX  
XX 12-MAR-2001; 2001WO-US07931.  
XX  
XX 10-MAR-2000; 2000US-188301P.  
PR 09-MAR-2001; 2001US-0802370.  
XX  
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
XX  
XX Van Nest G;  
XX  
XX WPI; 2002-049000/06.  
XX  
XX Reducing viremia and blood levels of hepatitis virus antigen in an  
PT individual infected with hepatitis B virus, comprises administering a  
PT composition comprising a polynucleotide having an immunostimulatory  
PT sequence -  
XX  
XX Disclosure; Page 20; 43pp; English.  
XX  
XX The present invention describes a method for reducing viraemia or blood  
CC levels of a hepatitis virus antigen in an individual infected with  
CC hepatitis B virus (HBV). The method comprises administering a composition  
CC comprising a polynucleotide having an immunostimulatory sequence (ISS)  
CC to the individual, where the ISS comprises the sequence 5'-C, G-3', an  
CC HBV antigen is not administered in conjunction with administration of  
CC the composition, and where the composition is administered in an amount  
CC sufficient to reduce HBV viraemia or blood levels of a hepatitis virus  
CC antigen. ISS has virucide, anti-inflammatory and hepatotropic activities,  
CC and can be used in gene therapy. The method can be used for suppressing  
CC and/or ameliorating hepatitis infection in an individual, especially for  
CC preventing, palliating, ameliorating, reducing and/or eliminating one or  
CC more symptoms of HBV or HCV (hepatitis C virus) infection without  
CC administering HBV or HCV antigens. The method is specifically useful for  
CC reducing viraemia and hepatitis viral antigen in blood. ISS-containing  
CC polynucleotides may also be used to improve physical symptoms such as  
CC jaundice, fatigue, abdominal pain, and other clinical/laboratory  
CC findings associated with hepatitis such as blood levels of liver enzymes,  
CC portal hypertension, or cirrhosis. The present sequence represents an  
CC ISS oligonucleotide given in the exemplification of the present  
CC invention.  
XX  
XX Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;  
SQ  
Query Match 71.4%; Score 15; DB 24; Length 22;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20  
|||  
Db 8 GAACGTTGAGATGA 22

RESULT 60  
AAS15592  
ID AAS15592 standard; DNA; 22 BP.  
XX  
XX AAS15592;  
AC

XX 29-JAN-2002 (first entry)  
 XX Immunostimulatory oligonucleotide (ISS-ODN) #1.  
 DE Immunostimulatory oligonucleotide (ISS-ODN) #1.  
 XX Immunostimulatory oligonucleotide; ISS-ODN; anti-allergic; antibacterial;  
 KM virucide; fungicide; vaccine; immunogen; plant allergen; ragweed;  
 KM grass pollen; food; latex; cat dander; cockroach; house dust mite;  
 KM pathogenic parasite; ss.  
 XX Synthetic.  
 OS  
 XX WO200176642-A1.  
 PN 18-OCT-2001.  
 PD 06-APR-2001; 2001WO-US11290.  
 XX 07-APR-2000; 2000US-195890P.  
 PR 07-APR-2000; 2000US-195890P.  
 XX (REGC ) UNIV CALIFORNIA.  
 PA Raz E, Takabayashi K, Nguyen M;  
 PI WPI; 2002-02586/03.  
 DR  
 XX New polynucleotide vaccine for eliciting immune response to an antigen  
 PT derived from a pathogen, plant or food, comprises antigen-encoding  
 PT nucleic acid sequence derived from non-host species of first phylum or  
 PT kingdom -  
 XX Example 4; Page 43; 64pp; English.  
 PS  
 XX The invention relates to a polynucleotide vaccine (I) comprising a  
 CC nucleic acid sequence encoding an antigen derived from a non-host species  
 CC of a first phylum or first kingdom, where the nucleic acid sequence  
 CC encoding the antigen is modified by deletion of a native signal sequence,  
 CC and/or an immunomodulatory nucleic acid sequence. (I) is useful for  
 CC modulating an immune response to an antigen, especially a plant (ragweed  
 CC or grass pollen), food, latex, cat dander, cockroach, or house dust mite  
 CC allergen. (I) is also useful for eliciting an immune response to an  
 CC antigen derived from a pathogen, such as bacterium, virus or a parasite.  
 CC The vaccine is co-administered with an immunostimulatory nucleotide.  
 CC sequence which comprises an unmethylated 5'-CG-3' nucleotide sequence.  
 CC Antigen of pathogenic parasites include Plasmodium, Leishmania, fungal,  
 CC yeast or other pathogens. The present sequence represents  
 CC immunostimulatory oligonucleotide (ISS-ODN) #1 which is co-injected  
 CC with (I) to amplify the immune response to the co-administered allergen.  
 CC  
 XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;  
 SQ  
 Query Match 71.4%; Score 15; DB 24; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
 |||||  
 DB 8 GAACGTCGAGATGA 22

RESULT 61  
 ABZ77582  
 ID ABZ77582 standard; DNA; 22 BP.  
 AC ABZ77582;  
 XX  
 DT 03-JUN-2003 (first entry)  
 XX  
 DE Nucleotide sequence of a control immunostimulatory oligonucleotide.  
 XX Immunomodulatory composition; immune response; Th2-type immune response;  
 KM allergy; asthma; infectious disease; vaccine; cancer; IFN-alpha;  
 KM IFN-gamma; idiopathic pulmonary fibrosis; scleroderma;

KM cutaneous radiation-induced fibrosis; hepatic fibrosis; renal fibrosis;  
 KM viral infection; mycobacterial disease; malaria; leishmaniasis;  
 KM toxoplasmosis; schistosomiasis; clonorchiasis; ss.  
 OS Synthetic.  
 XX WO2003014316-A2.  
 PN 20-FEB-2003.  
 PD 07-AUG-2002; 2002WO-US25123.  
 PF 07-AUG-2001; 2001US-310743P.  
 PR 25-OCT-2001; 2001US-335263P.  
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
 PA Fearon KL, Dina D;  
 PI WPI; 2003-248016/25.  
 DR  
 XX Immunomodulatory composition for modulating immune response and  
 PT reducing levels of immunoglobulin E in an individual having the related  
 PT disorder, has a complex of microcarrier and an immunomodulatory  
 PT oligonucleotide -  
 XX Example 3; Page 62; 79pp; English.  
 PS  
 XX The specification describes an immunomodulatory composition, which  
 CC comprises a complex of a microcarrier and an immunomodulatory  
 CC oligonucleotide which is three to six nucleotides in length and which  
 CC does not have a sequence selected from 5'-GACGTT-3', 5'-TCCGA-3', and  
 CC 5'-GAGCTT-3'. The composition is useful for modulating an immune  
 CC response in an individual suffering from a disorder associated with a  
 CC Th2-type immune response which is selected from allergies and  
 CC allergy-induced asthma, asthma or infectious disease. The individual  
 CC receives a prophylactic or therapeutic vaccine, where the therapeutic  
 CC vaccine is selected from an epitope which is selected from an allergy  
 CC epitope, a mycobacterial epitope, and a tumour-associated epitope. The  
 CC individual is at a risk of exposure to an infectious agent or at risk  
 CC of developing cancer, or suffers from cancer or an infectious disease.  
 CC The composition is useful for increasing interferon (IFN)-gamma or  
 CC IFN-alpha in an individual, where the individual suffers from a disorder  
 CC selected from idiopathic pulmonary fibrosis, scleroderma, cutaneous  
 CC radiation-induced fibrosis, hepatic fibrosis, and renal fibrosis, viral  
 CC infections and cancer. The composition is also useful for ameliorating  
 CC one or more symptoms of an infectious disease in an individual, where  
 CC the infectious disease is caused by a cellular pathogen. The infectious  
 CC disease is selected from mycobacterial disease, malaria, leishmaniasis,  
 CC toxoplasmosis, schistosomiasis, and clonorchiasis. The present sequence  
 CC represents an immunostimulatory oligonucleotide, used as a control in  
 CC the course of the invention.  
 CC  
 XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;  
 SQ  
 Query Match 71.4%; Score 15; DB 25; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
 |||||  
 DB 8 GAACGTCGAGATGA 22

RESULT 62  
 AAL51531  
 ID AAL51531 standard; DNA; 22 BP.  
 AC AAL51531;  
 XX  
 DT 10-APR-2003 (first entry)  
 XX  
 DE CTL recognition antigen-related oligonucleotide, SEQ ID No 5.

XX Cytotoxic T-lymphocyte recognition antigen; CTL recognition antigen;  
KV human T-lymphocytic leukemia virus-1; HTLV-1; tumour; health food;  
KW immune response-inducible vaccine; ds; primer; probe.  
XX Unidentified.  
XX WO200290981-A1.  
XX 14-NOV-2002.  
XX 02-MAY-2002; 2002WO-JP04406.  
XX 08-MAY-2001; 2001JP-0137526.  
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
XX Hanabuchi S, Ohashi T, Kannagi M;  
XX WPI; 2003-140232/13.  
XX Screening of cytotoxic T-lymphocyte-recognition antigen with a human  
PT T-lymphocytic leukemia virus-1 (HTLV-1) antitumor effect, for use as  
PT a vaccine, comprises administering a test substance to a  
PT HTLV-1-associated disease animal model -  
XX Example 10; Page 29; 53pp; Japanese.  
XX The invention comprises a method for screening a cytotoxic T-lymphocyte  
CC (CTL) recognition antigen, which includes CTLs with antitumor effect  
CC against human T-lymphocytic leukemia virus-1 (HTLV-1) tumours. The  
CC CTL-recognition antigens identified by the method of the invention are  
CC useful as immune response-inducible vaccines, and as components of drug  
CC preparations and health foods. The present DNA sequence represents an  
CC oligonucleotide that was used in an example of the invention.  
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;  
SQ  
Query Match 71.4%; Score 15; DB 25; Length 22;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 GAACGTCGAGATGA 20  
Db 8 GAACGTCGAGATGA 22  
RESULT 63  
AB257964  
ID AB257964 standard; DNA; 22 BP.  
XX  
AC AB257964;  
XX  
DT 14-APR-2003 (first entry)  
XX  
DE Immunostimulatory oligodeoxynucleotide ISS-ODN 1018.  
XX  
KW ISS-ODN 1018; immunostimulant; vaccine, adjuvant; phosphorothioate;  
KW gene therapy; liposome; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..22  
FT /\*tag= a  
FT /mod\_base= "OTHER"  
FT /note= "phosphorothioate linkage"  
XX  
PN WO2003000232-A2.  
XX  
PD 03-JAN-2003.  
XX  
PF 25-JUN-2002; 2002WO-IL00507.

XX 25-JUN-2001; 2001US-300072P.  
PR 17-DEC-2001; 2001US-339785P.  
XX  
XX (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Barenholz Y, Kedar E, Louria-Hayon Y, Joseph A, Raz E;  
PI Takabayashi K;  
XX WPI; 2003-201371/19.  
XX  
DR Loading immunostimulatory oligodeoxynucleotides (ISS-ODNs) in liposomes  
PT useful for stimulating an immune response comprises solubilizing at  
PT least one liposome-forming lipid in a solvent and drying or  
PT freeze-drying the solution -  
XX  
XX Example; Page 19; 68pp; English.  
XX  
XX The present sequence is that of phosphorothioate immunostimulatory  
CC oligodeoxynucleotide (ISS-ODN) 1018. The invention provides a  
CC novel, fast and simple method of preparing liposomes efficiently  
CC loaded (i.e. at least 60% loading) with ISS-ODN. The method is  
CC based on drying a suspension of amphipathic material and then  
CC hydrating it with an aqueous solution containing the ISS-ODN,  
CC thereby entrapping it in liposomes formed from the lipid. The  
CC ISS-ODN is preferably an endotoxin-free ISS-ODN with a  
CC phosphorothioate or phosphodiester backbone. Liposomal ISS-ODN can  
CC be used e.g. as a vaccine adjuvant against pathogens and cancer, in  
CC the treatment or prevention of diseases caused by certain infectious  
CC microorganisms, in the treatment or prevention of allergic  
CC diseases, or to boost innate immunity. In examples of the  
CC invention, ISS-ODN 1018 was encapsulated in large multilamellar  
CC liposomes with up to 95% efficiency. The liposomal formulation was  
CC a considerably more potent parenteral adjuvant in mice than the  
CC soluble form of ISS-ODN, as shown in experiments with an influenza  
CC vaccine. Enhancement of the systemic humoral and cellular response  
CC was demonstrated by liposomal ISS-ODN 1018 co-administered with  
CC hepatitis B vaccine, and of the systemic humoral response when  
CC administered with tuberculosis vaccine. Liposomal ISS-ODN 1018 was  
CC also used as an adjuvant for a cancer (mammary carcinoma)  
CC vaccine, and activated resistance to Leishmaniasis when administered  
CC after infection.  
XX  
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;  
Query Match 71.4%; Score 15; DB 25; Length 22;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 GAACGTCGAGATGA 20  
Db 8 GAACGTCGAGATGA 22  
RESULT 64  
AAV80098/C  
ID AAV80098 standard; DNA; 23 BP.  
XX  
AC AAV80098;  
XX  
DT 12-MAR-1999 (first entry)  
XX  
DE Immunomodulatory oligo comprising an ISS sequence.  
XX  
XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;  
KW ISS; cancer; allergy; asthma; hepatitis B infection; papillomavirus;  
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;  
KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.  
XX  
OS Synthetic.  
XX  
PN WO9855495-A2.

XX 10-DEC-1998.  
PD  
XX 05-JUN-1998; 98WO-US11578.  
PF  
XX 06-JUN-1997; 97US-0048793.  
PR  
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
PA  
XX Dina D, Roman M, Schwartz D;  
PI  
XX WPI; 1999-059898/05.  
DR  
XX Immunostimulatory oligonucleotides regulate the immune system - and  
PT contain an immune-stimulating octanucleotide sequence; for treating  
PT cancer, allergic and infectious diseases  
XX  
PS Claim 6; Page 29; 63pp; English.  
XX  
XX The invention relates to immunomodulatory oligonucleotides that comprise  
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS  
CC sequences are selected from the group consisting of AACGTTCC, AACGTTCC,  
CC GAGTTCC, and GAGTTCC. The immunomodulatory sequences are used to treat  
CC patients needing immune regulation, such as those suffering from cancer,  
CC an allergic disease and asthma. They are also used to prevent infectious  
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency  
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and  
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and  
CC Schistosoma. The immunomodulatory sequences are used to screen for human  
CC immunostimulatory activity by incubating macrophage cells and the  
CC oligonucleotide; and determining the relative amount of Th1-biased  
CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent  
CC specific claimed examples of such immunomodulatory oligonucleotides.  
XX  
SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;  
Query Match 71.4%; Score 15; DB 20; Length 23;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 GAACGTTGAGATGA 20  
DB 15 GAACGTTGAGATGA 1  
RESULT 65  
AA38067/C  
ID AAA38067 standard; DNA; 23 BP.  
AC  
XX AAA38067;  
XX  
XX 24-AUG-2000 (first entry)  
DT  
XX Immunostimulatory sequence (ISS) #3.  
DE  
XX Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;  
KW gp120; human immunodeficiency virus; HIV; immune response; infection;  
KW development; ss.  
XX  
XX Synthetic.  
OS  
XX WO200021556-A1.  
XX  
XX 20-APR-2000.  
PD  
XX 08-OCT-1999; 99WO-US23677.  
PF  
XX 09-OCT-1998; 98US-0103733.  
PR  
XX 07-OCT-1999; 99US-0415186.  
XX  
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
PA  
XX Tighe H, Raz E, Schwartz D, Takabayashi K;  
PI

XX WPI; 2000-317846/27.  
DR  
XX Anti-HIV composition comprises immunostimulatory polynucleotides and  
PT HIV glycoprotein gp120 useful for modulating, stimulating an immune  
PT response against HIV in an HIV infected individual -  
PT  
XX Disclosure; Page 16; 65pp; English.  
XX  
XX The present invention relates to an immunostimulatory composition  
CC comprising a human immunodeficiency virus (HIV) antigen, and an  
CC immunomodulatory polynucleotide comprising an immunostimulatory sequence  
CC (ISS). This sequence represents an ISS that can be used in the  
CC composition. An immunostimulatory composition which comprises a gp120  
CC conjugated to it and not conjugated, is used for modulating or  
CC stimulating a specific immune response against gp120 in an individual by  
CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It  
CC is also used for suppressing or delaying development of HIV infection in  
CC an individual infected with HIV or an individual at risk of infection in  
CC with HIV, respectively. It is also used for treating an individual  
CC infected with HIV in need of immune modulation.  
XX  
SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;  
Query Match 71.4%; Score 15; DB 21; Length 23;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 GAACGTTGAGATGA 20  
DB 15 GAACGTTGAGATGA 1  
RESULT 66  
AA314666/C  
ID AA314666 standard; DNA; 23 BP.  
AC  
XX AA314666;  
XX  
XX 18-DEC-2001 (first entry)  
DT  
XX Immunostimulatory sequence, ISS #3.  
DE  
XX Immunostimulatory sequence; ISS; ds; antiviral; immunogen;  
KW respiratory syncytial virus; RSV; influenza virus; rhinovirus;  
KW adenovirus; measles virus; mumps virus; parainfluenza virus;  
KW rubella virus; poxvirus; parvovirus; hantavirus; varicella virus.  
XX  
XX Respiratory syncytial virus.  
OS  
XX Synthetic.  
OS  
XX WO200168116-A2.  
XX  
XX 20-SEP-2001.  
PD  
XX 12-MAR-2001; 2001WO-US07839.  
PF  
XX 10-MAR-2000; 2000US-188583P.  
PR  
XX 09-MAR-2001; 2001US-0802686.  
XX  
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
PA  
XX Van Nest G;  
PI  
XX WPI; 2001-607438/69.  
DR  
XX Suppressing a respiratory syncytial virus infection by administering an  
PT immunostimulatory sequence at the site of infection is useful to  
PT prevent and treat lower respiratory tract viral infections -  
XX  
PS Disclosure; Page 15; 40pp; English.  
XX

CC The invention relates to suppressing a respiratory syncytial virus (RSV) infection in an exposed individual, comprising administering a polynucleotide comprising an immunostimulatory sequence (ISS) comprising the sequence 5'-C, G-3', where an RSV antigen is not administered.

CC The invention is used to prevent and treat respiratory syncytial virus infection of the lower respiratory tract and other viruses including influenza virus, rhinovirus, adenovirus, measles virus, mumps virus, parainfluenza virus, rubella virus, poxvirus, parvovirus, hantavirus and varicella virus. A kit for carrying out the administration is also included. Unlike the prior art antiviral agent ribavirin, which is a potential teratogen, the invention provides a treatment which does not carry unacceptable side effects. Other prior art medications treat the symptoms only, whilst the invention treats the infection. The present sequence is an ISS of the invention.

CC  
XX

SEQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 22; Length 23;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20  
DB 15 GAACGTTGAGATGA 1

RESULT 67  
AAH75994/C  
ID AAH75994 standard; DNA; 23 BP.  
AC AAH75994;  
XX  
DT 15-NOV-2001 (first entry)  
XX  
DE Immunomodulatory oligonucleotide #3.  
XX  
KW Immunomodulatory; immunostimulatory; Th1-type immune response;  
KW Th2-type immune response; interferon; idiopathic pulmonary fibrosis;  
KW viral infection; ss.  
XX  
OS Synthetic.  
XX  
PN WO200168143-A2.  
XX  
PD 20-SEP-2001.  
XX  
PF 12-MAR-2001; 2001WO-US07843.  
XX  
PR 10-MAR-2000; 2000US-0188557.  
PR 09-MAR-2001; 2001US-0802376.  
XX  
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
XX  
PI Van Nest G, Tuck S;  
PI WPI; 2001-582389/65.  
XX  
DR Immunomodulatory polynucleotide/microcarrier complexes comprise an immunostimulatory sequence containing polynucleotide linked to a nonbiodegradable microcarrier -  
XX  
PS Disclosure; Page 18; 61pp; English.  
XX  
CC The present invention relates to immunomodulatory polynucleotide/microcarrier complexes. The complexes comprise an immunostimulatory sequence (ISS), e.g. the present sequence, linked to a nonbiodegradable microcarrier provided that if the microcarrier is gold, latex or magnetic then the linkage is not biotin/avidin. The complex is useful for modulating an immune response (especially stimulating a Th1-type response or suppressing a Th2-type response), increasing interferon-gamma (especially in a patient suffering from idiopathic pulmonary fibrosis), increasing interferon-alpha (especially in patients suffering from viral infection) and reducing levels of IgE.

XX  
SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 22; Length 23;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20  
DB 15 GAACGTTGAGATGA 1

RESULT 68  
AAH41575/C  
ID AAH41575 standard; DNA; 23 BP.  
AC AAH41575;  
XX  
DT 24-AUG-2001 (first entry)  
XX  
DE Immunostimulatory sequence (ISS) SEQ ID NO:3.  
XX  
KW Immunostimulatory sequence; ISS; immunomodulatory; immune response;  
KW antigen; antiallergic; modulation; Th1 lymphocyte stimulation; allergy;  
KW Th1-associated cytokine; Th2 lymphocyte suppression; cytokine; ss.  
XX  
OS Synthetic.  
XX  
PN WO200135991-A2.  
XX  
PD 25-MAY-2001.  
XX  
PF 15-NOV-2000; 2000WO-US31385.  
XX  
PR 15-NOV-1999; 99US-0165467.  
PR 14-NOV-2000; 2000US-0713136.  
XX  
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
XX  
PI Tuck S, Van Nest G;  
PI WPI; 2001-329209/34.  
XX  
DR Populations of conjugate molecules comprising polynucleotide  
XX  
PT Immunostimulatory sequences polynucleotides and antigens, useful for  
PT controlling immune responses -  
XX  
PS Disclosure; Page 30; 97pp; English.  
XX  
CC The present invention describes immunomodulatory populations (I) and (II) of conjugate molecules (Cm) comprising immunostimulatory sequences (ISS) of polynucleotides and antigens. The extent of conjugation affects the immunological properties (e.g. the extent of antigen-specific antibody formation, including Th1-associated antibody formation) so the conjugates are used for altering the type and extent of immune response. (I) and (II) have immunomodulatory, immunosuppressive and antiallergic activities, and can be used in the modulation of immune responses via the stimulation of Th1 lymphocytes and Th1-associated cytokines, and suppression of Th2 lymphocytes and cytokines. The populations (I) and (II) of conjugate molecules may be used for modulating immune responses in individuals e.g. for the treatment of an allergic condition. (I) and (II) may be used to modulate immune responses and therefore prevent potentially harmful reactions to antigens. The present sequence represents an ISS polynucleotide which is used in the exemplification of the present invention.

CC  
XX

SEQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 22; Length 23;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20

Db 15 GAACGTTGAGATGA 1

|||||

RESULT 69  
AAFT7042/C  
ID AAF77042 standard; DNA; 23 BP.

AAFT7042;  
AC  
XX  
XX  
DT 15-MAY-2001 (first entry)  
DE Immunostimulatory DNA #2.  
XX  
XX  
KW Modulate; immune; antigen; immunostimulatory; ds.  
XX  
OS Synthetic.  
XX  
PN WO200112223-A2.  
XX  
PD 22-FEB-2001.  
XX  
PP 18-AUG-2000; 2000WO-US22835.  
XX  
PR 19-AUG-1999; 99US-0149768.  
XX  
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
XX  
PI Van Nest G;  
XX  
DR WPI; 2001-211136/21.  
XX  
PT Modulating immune response to a second antigen in humans involves  
PT administering an immunostimulatory polynucleotide comprising an  
PT immunostimulatory sequence and a first antigen  
XX  
PS Disclosure; Page 15; 63pp; English.  
XX  
CC The present invention relates to modulating an immune response to  
CC a second antigen in an individual, involving  
CC administering to the individual an immunomodulatory polynucleotide  
CC comprising an immunostimulatory sequence (ISS) and a first antigen.  
XX  
SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 22; Length 23;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20  
Db 15 GAACGTTGAGATGA 1

RESULT 70  
AAS16339/C  
ID AAS16339 standard; DNA; 23 BP.  
XX  
AC AAS16339;  
XX  
DT 14-FEB-2002 (first entry)  
XX  
DE ISS polynucleotide #3 useful for treating herpes virus infections.  
XX  
KW Herpes simplex virus; HSV infection; immunostimulatory sequence; ISS;  
KW immune response; alphaherpesvirinae; herpes virus zoster virus; VZV;  
KW HSV-1; HSV-2; chicken pox; herpes labialis; cold sore; genital herpes;  
KW virucide; ss.  
XX  
OS Synthetic.  
XX  
PN WO200168103-A2.  
XX

PD 20-SEP-2001.  
XX  
XX 12-MAR-2001; 2001WO-US07841.  
XX  
XX 10-MAR-2000; 2000US-188556P.  
XX 09-MAR-2001; 2001US-0802518.  
XX  
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
XX  
XX  
PI Van Nest G;  
XX  
DR WPI; 2002-041171/05.  
XX  
XX  
PT Preventing, reducing the severity or reducing the recurrence of an  
PT infection or symptom of herpes simplex virus (HSV), e.g. HSV-2,  
PT comprises administering an immunostimulatory sequence to an individual  
XX  
XX  
PS Disclosure; Page 19; 49pp; English.  
XX  
XX The present invention relates to novel methods of treating, preventing,  
XX or reducing the severity or recurrence of a symptom of herpes simplex  
XX virus (HSV) infection in an individual who has been exposed to or who is  
XX infected with HSV. The method comprises administering a polynucleotide  
XX having an immunostimulatory sequence (ISS; AAS16337-AAS16345) which  
XX induces an immune response. A composition containing ISS is administered  
XX without a HSV (alphaherpesvirinae) antigen. The composition of HSV  
XX infection caused by herpes virus zoster virus (VZV), HSV-1 and  
XX particularly HSV-2. Such HSV infections include chicken pox, herpes  
XX labialis (cold sores) and genital herpes. The present sequence represents  
XX one of the ISS polynucleotides of the invention.  
XX Note: The present sequence is shown as single stranded in the  
XX specification, but the patentees state on page 20 that this sequence may  
XX be double stranded.

Query Match 71.4%; Score 15; DB 24; Length 23;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20  
Db 15 GAACGTTGAGATGA 1

RESULT 71  
AAS16350/C  
ID AAS16350 standard; DNA; 23 BP.  
XX  
AC AAS16350;  
XX  
DT 14-FEB-2002 (first entry)  
XX  
DE ISS polynucleotide #3 useful for treating papillomavirus infections.  
XX  
XX Animal papillomavirus infection; human papillomavirus; HPV; STD; wart;  
XX sexually transmitted disease; cervical cancer; immune response;  
KW immunostimulatory sequence; ISS; virucide; ss.  
XX  
OS Synthetic.  
XX  
PN WO200168117-A2.  
XX  
PD 20-SEP-2001.  
XX  
PP 12-MAR-2001; 2001WO-US07842.  
XX  
PR 10-MAR-2000; 2000US-188265P.  
XX 09-MAR-2001; 2001US-0802445.  
XX  
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
XX



XX	Van Nest G.
PI	WPI: 2002-041172/05.
DR	
XX	Treating, preventing or ameliorating papillomavirus infections,
PT	comprises administering a composition comprising a polynucleotide
PT	having an immunostimulatory sequence to the individual
XX	
PS	Disclosure; Page 20; 44pp; English.
XX	
CC	The present invention relates to novel methods of treating, preventing,
CC	or reducing the severity or recurrence of a symptom of papillomavirus
CC	infection in an individual that has been exposed to or who is infected
CC	with papillomavirus. The method comprises administering a polynucleotide
CC	having an immunostimulatory sequence (ISS; AAS16348-AAS16355) which
CC	induces an immune response. A composition containing ISS is administered
CC	without a papillomavirus antigen. The composition can be included in a
CC	kit for ameliorating or preventing a symptom of human or animal
CC	papillomavirus infection. Infections with human papillomavirus (HPV)
CC	which can be prevented or treated using the method of the invention
CC	include sexually transmitted diseases (STDs), warts, papillomas and
CC	cerical cancer. The present sequence represents one of the ISS
CC	polynucleotides of the invention.
CC	Note: The present sequence is shown as single stranded in the
CC	specification, but the patentees state on page 20 that this sequence may
CC	be double stranded.
XX	
SO	Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;
Query Match	71.4%; Score 15; DB 24; Length 23;
Best Local Similarity	100.0%; Pred. No. 19;
Matches 15; Conservative	0; Mismatches 0; Indels 0; Gaps 0.
Oy	6 GAACGTCGAGATGA 20
Db	15 GAACGTCGAGATGA 1
RESULT 72	
AAD21879	
ID	AAD21879 standard; DNA; 23 BP.
XX	
AC	AAD21879;
XX	
DT	12-FEB-2002 (first entry)
XX	
DE	Immunostimulatory sequence oligonucleotide (ISS-ODN) #2.
XX	
KW	Cytotoxic T lymphocyte; CTL; T cell; tumour load; cancer radiotherapy;
KW	immunostimulatory sequence oligonucleotide; ISS-ODN; chemotherapy;
KW	immunosuppression; transplantation; autoimmune disease; infection;
KW	acquired immune deficiency syndrome; AIDS; intracellular pathogen;
KW	cytomegalovirus; mycobacterial infection; Epstein-Barr virus;
KW	varicella zoster virus; human immunodeficiency virus; HIV;
KW	phosphorochioste backbone; ss.
XX	
OS	Unidentified.
XX	
PH	Key
FT	modified_base
FT	1.22
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "Phosphorochioste backbone"
FT	23
FT	/tag= b
FT	/note= "This residue is not found in the sequence
XX	shown in page 44 of the specification"
PN	WO200172123-A1.
XX	
PD	04-OCT-2001.
XX	

Pf	28-MAR-2001; 2001WO-US10118.
Xx	
Pr	28-MAR-2000; 2000US-192537P.
Pr	11-MAY-2000; 2000US-203567P.
Pr	05-JUL-2000; 2000US-215895P.
Xx	
Pa	(REGC ) UNIV CALIFORNIA.
Pa	(VERE-) DEPT VETERANS AFFAIRS.
Xx	
Pt	Raz E, Cho HJ, Richman DD, Horner AA;
Pt	WPI; 2002-010699/01.
Xx	
Pt	Increasing antigen-specific cytotoxic T lymphocyte activity in a CD4+ T
Pt	cell deficient individual, useful to treat immunodeficiency and block
Pt	HIV infection, comprises administering immunostimulatory nucleic acid
Pt	-
Xx	
Ps	Example 1; Page 53; 91pp; English.
Xx	
Cc	The present invention relates to a method for increasing antigen-specific
Cc	cytotoxic T lymphocyte (CTL) activity in a CD4+ T cell-deficient
Cc	individual, comprising administering an immunostimulatory sequence
Cc	oligonucleotide (ISS-ODN). The immunostimulatory nucleic acids of the
Cc	invention are used in CD4+ T cell-deficient individuals to decrease
Cc	tumor load, to treat a primary or acquired immunodeficiency,
Cc	particularly where the acquired immunodeficiency is temporary and due
Cc	to cancer radiotherapy or chemotherapy or immunosuppression following
Cc	bone marrow or organ transplantation, or autoimmune disease treatment,
Cc	or is acquired immunodeficiency syndrome (AIDS). The nucleic acids may
Cc	be used to treat a person at risk of becoming CD4+ T cell-deficient,
Cc	particularly where someone at risk of cancer recurrence. They are also
Cc	used to treat infection, particularly by an intracellular pathogen,
Cc	especially one caused by cytomegalovirus, Mycobacterium tuberculosis,
Cc	M. avium, Epstein-Barr virus, a fungus Yeast, varicella zoster virus or
Cc	human immunodeficiency virus (HIV). The present sequence is a
Cc	phosphorothioate immunostimulatory sequence oligonucleotide (ISS-ODN),
Cc	used in the exemplification of the invention.
Xx	
Sq	Sequence 23 BP; 6 A; 3 C; 7 G; 6 T; 1 other;
Query Match	71.4%; Score 15; DB 24; Length 23;
Beet Local Similarity	100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	6 GAACGTCGAGATGA 20       8 GAACGTCGAGATGA 22
Db	
RESULT 73	
ABA03835/C	
ID	ABA03835 standard; DNA; 23 BP.
Ac	ABA03835;
Xx	
Dt	12-FEB-2002 (first entry)
Xx	
DE	Immunostimulatory sequence (ISS) SEQ ID NO:3.
Xx	
Kw	immunomodulatory polynucleotide/microcarrier complex; INF/MC; IgE;
Kw	immunomodulation; immunostimulation; phosphorothioate; immunomodulator;
Kw	antiallergic; antibacterial; antiprotocozal; antiparasitic; hepatotropic;
Kw	nephroretic; interferon-alpha stimulator; interferon-gamma stimulator;
Kw	immunoglobulin B stimulator; immune response; IPF; scleroderma; malaria;
Kw	idiopathic pulmonary fibrosis; cutaneous radiation-induced fibrosis;
Kw	hepatic fibrosis; renal fibrosis; infectious disease; leishmaniasis;
Kw	mycobacterial disease; toxoplasmosis; schistosomiasis; chlamorchiasis;
Kw	allergy; allergy-induced asthma; prophylactic vaccine; cancer; ss.
Xx	
Os	Synthetic.
Xx	
Pn	WO200168144-A2.

XX 20-SEP-2001.  
PD 12-MAR-2001; 2001WO-US07848.  
XX PF 10-MAR-2000; 2000US-188303P.  
XX PR 09-MAR-2001; 2001US-0802359.  
XX PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
XX PI Van Nest G, Tuck S;  
XX DR WPI; 2002-049002/06.  
PT New immunomodulatory polynucleotide/microcarrier complex, useful for  
PT modulating the immune response of individuals, particularly humans, or  
PT for treating idiopathic pulmonary fibrosis, scleroderma, malaria or  
PT allergies -  
PS Disclosure; Page 18; 63pp; English.  
XX The present invention describes an immunomodulatory polynucleotide/  
XX microcarrier (IMP/MC) complex (I), which comprises a polynucleotide  
XX having an immunostimulatory sequence (ISS) linked to a biodegradable  
XX microcarrier (MC). The ISS comprises the sequence: 5'-CG-3', where the  
XX MC is less than 10 microm in size. (I) has immunomodulatory,  
XX antiallergic, antibacterial, antiparasitic, hepatotropic  
XX and nephrotropic activities. It can be used as an interferon (IFN)-alpha  
XX stimulator, IFN-gamma stimulator or an immunoglobulin E (IGE) stimulator.  
XX (I) can be used for modulating the immune response of individuals,  
XX particularly humans. The IMP/MC complex is particularly useful for  
XX treating idiopathic pulmonary fibrosis (IPF), scleroderma, cutaneous  
XX radiation-induced fibrosis, hepatic fibrosis including  
XX schistosomiasis-induced hepatic fibrosis, renal fibrosis, infectious  
XX diseases caused by cellular pathogen (e.g. a mycobacterial disease,  
XX malaria, leishmaniasis, toxoplasmosis, schistosomiasis or  
XX chlamydia), or disorders associated with a Th2-type immune  
XX response (e.g. allergies or allergy-induced asthma). The IMP/MC may  
XX also be used in individuals receiving therapeutic or prophylactic  
XX vaccines, in individuals suffering from cancer, or in individuals at  
XX risk of exposure to an infectious agent. The present sequence represents  
XX an ISS given in the exemplification of the present invention.  
XX  
SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;  
Query Match 71.4%; Score 15; DB 24; Length 23;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 6 GAACGTCGAGATGA 20  
DB 15 GAACGTCGAGATGA 1  
RESULT 74  
ABA03846/C  
ID ABA03846 standard; DNA; 23 BP.  
XX ABA03846;  
AC  
XX 12-FEB-2002 (first entry)  
XX  
XX Immunostimulatory sequence (ISS) SEQ ID NO:3.  
XX  
XX Immunostimulatory sequence; ISS; immunostimulation; viral infection;  
XX immunomodulation; virucide; gene therapy; viraemia; ss.  
XX  
XX Synthetic.  
XX  
XX WO200168077-A2.  
XX  
XX 20-SEP-2001.  
XX

PF 12-MAR-2001; 2001WO-US07840.  
XX 10-MAR-2000; 2000US-188302P.  
XX PR 09-MAR-2001; 2001US-0802685.  
XX PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
XX PI Van Nest G;  
XX DR WPI; 2002-048999/06.  
XX  
XX Reducing severity, recurrence or duration of symptom of virus  
XX infection, or reducing viremia or blood levels of virus antigen,  
XX comprises administering a polynucleotide having an immunostimulatory  
XX sequence -  
PS Disclosure; Page 20; 65pp; English.  
XX The present invention describes a method for reducing severity of a  
XX symptom of virus infection in an individual infected with a virus. The  
XX method comprises administering a composition consisting of a  
XX polynucleotide having an immunostimulatory sequence (ISS). The ISS  
XX comprises the sequence 5'-C/G,pyrimidine,pyrimidine,C/G-3'. An antigen  
XX is administered in conjunction with the composition. ISS has virucide  
XX activity and can be used in gene therapy. The method using the ISS can  
XX be used for suppressing, ameliorating and/or preventing viral infections  
XX to an individual who may be at risk of being exposed to, exposed to or  
XX infected by a virus. It may also be used in reducing the recurrence  
XX or duration of a symptom of viral infection, delaying the development  
XX of a virus infection, and reducing viraemia or blood levels of virus  
XX antigens. The present sequence represents an ISS given in the  
XX exemplification of the present invention.  
XX  
SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;  
Query Match 71.4%; Score 15; DB 24; Length 23;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 6 GAACGTCGAGATGA 20  
DB 15 GAACGTCGAGATGA 1  
RESULT 75  
ABA03858/C  
ID ABA03858 standard; DNA; 23 BP.  
XX ABA03858;  
AC  
XX 12-FEB-2002 (first entry)  
XX  
XX Immunostimulatory sequence (ISS) SEQ ID NO:3.  
XX  
XX Immunostimulatory sequence; ISS; immunomodulation; HBV; HCV; infection;  
XX hepatitis B virus; hepatitis C virus; virucide; anti-inflammatory;  
XX hepatotropic; gene therapy; hepatitis infection; viraemia; jaundice;  
XX fatigue; abdominal pain; portal hypertension; cirrhosis; ss.  
XX  
XX Synthetic.  
XX  
XX WO200168078-A2.  
XX  
XX 20-SEP-2001.  
XX  
XX 12-MAR-2001; 2001WO-US07931.  
XX  
XX 10-MAR-2000; 2000US-188301P.  
XX PR 09-MAR-2001; 2001US-0802370.  
XX  
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.  
XX  
XX Van Nest G;  
XX

XX WPI: 2002-04900/06.  
DR  
XX

PT Reducing viremia and blood levels of hepatitis virus antigen in an  
PT individual infected with hepatitis B virus, comprises administering a  
PT composition comprising a polynucleotide having an immunostimulatory  
PT sequence -  
XX  
XX

PS Disclosure: Page 20; 43pp; English.

CC The present invention describes a method for reducing viraemia or blood  
CC levels of a hepatitis virus antigen in an individual infected with  
CC hepatitis B virus (HBV). The method comprises administering a composition  
CC comprising a polynucleotide having an immunostimulatory sequence (ISS)  
CC to the individual, where the ISS comprises the sequence 5'-C<sub>1</sub>-G-3', an  
CC HBV antigen is not administered in conjunction with administration of  
CC the composition, and where the composition is administered in an amount  
CC sufficient to reduce HBV viraemia or blood levels of a hepatitis virus  
CC antigen. ISS has virucide, anti-inflammatory and hepatotropic activities,  
CC and can be used in gene therapy. The method can be used for suppressing  
CC and/or ameliorating hepatitis infection in an individual, especially for  
CC preventing, palliating, ameliorating, reducing and/or eliminating one or  
CC more symptoms of HBV or HCV (hepatitis C virus) infection without  
CC administering HBV or HCV antigens. The method is specifically useful for  
CC reducing viraemia and hepatitis viral antigen in blood. ISS-containing  
CC polynucleotides may also be used to improve physical symptoms such as  
CC jaundice, fatigue, abdominal pain, and other clinical/laboratory  
CC findings associated with hepatitis such as blood levels of liver enzymes,  
CC portal hypertension, or cirrhosis. The present sequence represents an  
CC ISS oligonucleotide given in the exemplification of the present  
CC invention.  
XX  
XX

SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 24; Length 23;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
|||  
Db 15 GAACGTCGAGATGA 1

Search completed: December 17, 2003, 09:18:02  
Job time : 150 secs

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OM nucleic - nucleic search, using sw model

Run on: December 17, 2003, 09:38:49 : Search time 1152 Seconds  
(without alignments)  
60.743 Million cell updates/sec

Title: US-10-033-243-132

Perfect score: 21

Sequence: 1 tcgcgcacgtcgcgatgat 21

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 2211978 seqs, 1666101734 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4423956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	21	100.0	21	US-10-033-243-132	Sequence 132, App
2	19	90.5	19	US-09-927-422A-16	Sequence 16, Appl
3	19	90.5	19	US-10-176-883-41	Sequence 41, Appl
4	19	90.5	19	US-10-177-826-41	Sequence 41, Appl
5	19	90.5	19	US-10-033-243-19	Sequence 19, Appl
6	19	90.5	22	US-10-176-883-52	Sequence 52, Appl
7	19	90.5	22	US-10-033-243-30	Sequence 30, Appl
8	19	90.5	22	US-10-177-826-36	Sequence 36, Appl
9	16	76.2	18	US-10-177-826-36	Sequence 36, Appl
10	16	76.2	18	US-10-033-243-14	Sequence 14, Appl
11	16	76.2	18	US-10-176-883-13	Sequence 13, App
12	16	76.2	66	US-10-177-826-139	Sequence 139, App
13	16	76.2	66	US-09-848-986-21	Sequence 21, Appl
14	15	71.4	20	US-10-233-121A-21	Sequence 21, Appl
15	15	71.4	20	US-10-233-121A-21	Sequence 21, Appl

16	15	71.4	22	9	US-09-802-666-1	Sequence 1, Appl
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29	15	71.4	22	10	US-09-828-505-1	Sequence 1, Appl
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31	15	71.4	22	11	US-09-927-422A-1	Sequence 1, Appl
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33	15	71.4	22	11	US-09-738-046A-3	Sequence 3, Appl
34	15	71.4	22	11	US-09-927-884-1	Sequence 1, Appl
35	15	71.4	22	11	US-09-927-884-2	Sequence 2, Appl
36	15	71.4	22	13	US-09-802-359-1	Sequence 1, Appl
37	15	71.4	22	13	US-09-802-359-2	Sequence 2, Appl
38	15	71.4	22	13	US-09-967-864-19	Sequence 19, Appl
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52	15	71.4	22	13	US-10-176-883-141	Sequence 141, App
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57	15	71.4	22	13	US-10-177-826-79	Sequence 79, Appl
58	15	71.4	22	13	US-10-177-826-85	Sequence 85, Appl
59	15	71.4	22	13	US-10-177-826-85	Sequence 85, Appl
60	15	71.4	22	13	US-10-177-826-140	Sequence 140, App
61	15	71.4	22	13	US-10-177-826-141	Sequence 141, App
62	15	71.4	22	13	US-10-357-760-1	Sequence 1, Appl
63	15	71.4	22	13	US-10-357-760-2	Sequence 2, Appl
64	15	71.4	22	13	US-10-056-420-4	Sequence 4, Appl
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66	15	71.4	22	15	US-10-033-243-12	Sequence 12, Appl
67	15	71.4	22	15	US-10-033-243-40	Sequence 40, Appl
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75	15	71.4	22	15	US-10-229-117-52	Sequence 52, Appl
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85	15	71.4	22	15	US-10-229-117-52	Sequence 52, Appl
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90 14 66.7 14 13 US-10-176-883-98 Sequence 98, Appl
91 14 66.7 14 13 US-10-176-883-104 Sequence 104, Appl
92 14 66.7 14 13 US-10-177-826-98 Sequence 98, Appl
93 14 66.7 14 13 US-10-177-826-104 Sequence 104, Appl
94 14 66.7 14 13 US-10-033-243-98 Sequence 98, Appl
95 14 66.7 16 13 US-10-176-883-33 Sequence 33, Appl
96 14 66.7 16 13 US-10-176-826-33 Sequence 33, Appl
97 14 66.7 16 15 US-10-033-243-11 Sequence 11, Appl
98 14 66.7 18 13 US-10-176-883-51 Sequence 51, Appl
99 14 66.7 18 13 US-10-176-883-83 Sequence 83, Appl
100 14 66.7 18 13 US-10-177-826-51 Sequence 51, Appl
```

## ALIGNMENTS

```
RESULT 1
US-10-033-243-132 Application US/10033243
```

```
; Sequence 132, Application US/10033243
; Publication No. US20030049266A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: PEARON, Karen L.
```

```
; APPLICANT: Dina, Dino
```

```
; TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
```

```
; FILE REFERENCE: 37782001800
```

```
; CURRENT APPLICATION NUMBER: US/10/033,243
```

```
; PRIOR FILING DATE: 2002-04-03
```

```
; PRIOR APPLICATION NUMBER: 60/258,675
```

```
; PRIOR FILING DATE: 2000-12-27
```

```
; NUMBER OF SEQ ID NOS: 133
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 132
```

```
; LENGTH: 21
```

```
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
```

```
; OTHER INFORMATION: Polynucleotide containing CG
```

```
US-10-033-243-132
```

```
Query Match 100.0%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TCGTGAACGTTGAGATGAT 21
```

```
Db 1 TCGTGAACGTTGAGATGAT 21
```

```
RESULT 2
US-09-927-422A-16
```

```
; Sequence 16, Application US/09927422A
```

```
; Publication No. US20030022852A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Van Nest, Gary
```

```
; APPLICANT: Tuck, Stephen
```

```
; APPLICANT: Fearon, Karen L.
```

```
; TITLE OF INVENTION: BIODEGRADABLE IMMUNOMODULATORY
```

```
; FILE REFERENCE: 37782001420
```

```
; CURRENT APPLICATION NUMBER: US/09/927,422A
```

```
; PRIOR FILING DATE: 2001-08-10
```

```
; PRIOR APPLICATION NUMBER: U.S. 09/802,359
```

```
; PRIOR FILING DATE: 2001-03-09
```

```
; PRIOR APPLICATION NUMBER: U.S. 60/188,30
```

```
; NUMBER OF SEQ ID NOS: 23
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 16
```

```
; LENGTH: 19
```

```
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
```

```
US-09-927-422A-16
```

```
Query Match 90.5%; Score 19; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TCGTGAACGTTGAGATG 19
```

```
Db 1 TCGTGAACGTTGAGATG 19
```

```
RESULT 3
US-10-176-883-41
```

```
; Sequence 41, Application US/10176883
```

```
; Publication No. US20030175731A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Fearon, Karen
```

```
; APPLICANT: Dina, Dino
```

```
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
```

```
; FILE REFERENCE: 37782002000
```

```
; CURRENT APPLICATION NUMBER: US/10/176,883
```

```
; PRIOR FILING DATE: 2002-06-21
```

```
; PRIOR APPLICATION NUMBER: 60/299,883
```

```
; PRIOR FILING DATE: 2001-06-21
```

```
; PRIOR APPLICATION NUMBER: 60/375,253
```

```
; PRIOR FILING DATE: 2002-04-23
```

```
; NUMBER OF SEQ ID NOS: 141
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 41
```

```
; LENGTH: 19
```

```
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
```

```
; OTHER INFORMATION: Synthetic construct
```

```
US-10-176-883-41
```

```
Query Match 90.5%; Score 19; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TCGTGAACGTTGAGATG 19
```

```
Db 1 TCGTGAACGTTGAGATG 19
```

```
RESULT 4
US-10-177-826-41
```

```
; Sequence 41, Application US/10177826
```

```
; Publication No. US20030199466A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Fearon, Karen
```

```
; APPLICANT: Dina, Dino
```

```
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
```

```
; FILE REFERENCE: 37782002001
```

```
; CURRENT APPLICATION NUMBER: US/10/177,826
```

```
; PRIOR FILING DATE: 2002-06-21
```

```
; PRIOR APPLICATION NUMBER: 60/299,883
```

```
; PRIOR FILING DATE: 2001-06-21
```

```
; PRIOR APPLICATION NUMBER: 60/375,253
```

```
; PRIOR FILING DATE: 2002-04-23
```

```
; NUMBER OF SEQ ID NOS: 141
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 41
```

```
; LENGTH: 19
```

```
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
```

FEATURE:  
OTHER INFORMATION: Synthetic construct  
US-10-177-826-41

Query Match 90.5%; Score 19; DB 13; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.065;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCGTCGAACGTTCCGAGATG 19  
|||||  
Db 1 TCGTCGAACGTTCCGAGATG 19

RESULT 5  
US-10-033-243-19

Sequence 19, Application US/10033243  
Publication No. US20030049266A1  
GENERAL INFORMATION:

APPLICANT: FEARON, Karen L.

APPLICANT: DINA, Dino

TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND

TITLE OF INVENTION: METHODS OF USING THE SAME

FILE REFERENCE: 37782001800

CURRENT APPLICATION NUMBER: US/10/033,243

PRIOR FILING DATE: 2002-04-03

PRIOR APPLICATION NUMBER: 60/258,675

PRIOR FILING DATE: 2000-12-27

NUMBER OF SEQ ID NOS: 133

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 19

LENGTH: 19

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Polynucleotide containing CG

US-10-033-243-19

Query Match 90.5%; Score 19; DB 15; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.065;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCGTCGAACGTTCCGAGATG 19  
|||||  
Db 1 TCGTCGAACGTTCCGAGATG 19

RESULT 6  
US-10-176-883-52

Sequence 52, Application US/10176883  
Publication No. US20030175731A1  
GENERAL INFORMATION:

APPLICANT: FEARON, Karen

APPLICANT: DINA, Dino

APPLICANT: TUCK, Stephen

TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND

TITLE OF INVENTION: METHODS OF USING THE SAME-I

FILE REFERENCE: 37782002000

CURRENT APPLICATION NUMBER: US/10/176,883

PRIOR FILING DATE: 2002-06-21

PRIOR APPLICATION NUMBER: 60/299,883

PRIOR FILING DATE: 2001-06-21

PRIOR APPLICATION NUMBER: 60/375,253

PRIOR FILING DATE: 2002-04-23

NUMBER OF SEQ ID NOS: 141

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 52

LENGTH: 22

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic construct  
US-10-176-883-52

Query Match 90.5%; Score 19; DB 13; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.064;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCGTCGAACGTTCCGAGATG 19  
|||||  
Db 4 TCGTCGAACGTTCCGAGATG 22

RESULT 7  
US-10-177-826-52

Sequence 52, Application US/10177826  
Publication No. US20030199466A1  
GENERAL INFORMATION:

APPLICANT: FEARON, Karen

APPLICANT: DINA, Dino

APPLICANT: TUCK, Stephen

TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND

TITLE OF INVENTION: METHODS OF USING THE SAME-II

FILE REFERENCE: 37782002001

CURRENT APPLICATION NUMBER: US/10/177,826

PRIOR FILING DATE: 2002-06-21

PRIOR APPLICATION NUMBER: 60/299,883

PRIOR FILING DATE: 2001-06-21

PRIOR APPLICATION NUMBER: 60/375,253

PRIOR FILING DATE: 2002-04-23

NUMBER OF SEQ ID NOS: 141

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 52

LENGTH: 22

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic construct

US-10-177-826-52

Query Match 90.5%; Score 19; DB 13; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.064;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCGTCGAACGTTCCGAGATG 19  
|||||  
Db 4 TCGTCGAACGTTCCGAGATG 22

RESULT 8  
US-10-033-243-30

Sequence 30, Application US/10033243  
Publication No. US20030049266A1  
GENERAL INFORMATION:

APPLICANT: FEARON, Karen L.

APPLICANT: DINA, Dino

TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND

TITLE OF INVENTION: METHODS OF USING THE SAME

FILE REFERENCE: 37782001800

CURRENT APPLICATION NUMBER: US/10/033,243

PRIOR FILING DATE: 2002-04-03

PRIOR APPLICATION NUMBER: 60/258,675

PRIOR FILING DATE: 2000-12-27

NUMBER OF SEQ ID NOS: 133

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 30

LENGTH: 22

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Polynucleotide containing CG

Query Match 90.5%; Score 19; DB 15; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.064;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCGTGAACGTTTCGAGATG 19  
|||  
Db 4 TCGTGAACGTTTCGAGATG 22

## RESULT 9

US-10-176-883-36  
; Sequence 36, Application US/10176883  
; Publication No. US20030175731A1  
; GENERAL INFORMATION:  
; APPLICANT: Fearon, Karen  
; APPLICANT: Dina, Dino  
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND  
; FILE REFERENCE: 377882002000  
; CURRENT APPLICATION NUMBER: US/10/176,883  
; PRIOR FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: 60/299,883  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 60/375,253  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 36  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-10-176-883-36

Query Match 76.2%; Score 16; DB 13; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TCGAACGTTTCGAGATG 19  
|||  
Db 3 TCGAACGTTTCGAGATG 18

## RESULT 10

US-10-177-826-36  
; Sequence 36, Application US/10177826  
; Publication No. US2003019466A1  
; GENERAL INFORMATION:  
; APPLICANT: Fearon, Karen  
; APPLICANT: Dina, Dino  
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND  
; FILE REFERENCE: 377882002001  
; CURRENT APPLICATION NUMBER: US/10/177,826  
; PRIOR FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: 60/299,883  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 60/375,253  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 36  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-10-177-826-36

Query Match 76.2%; Score 16; DB 13; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TCGAACGTTTCGAGATG 19

Db 3 TCGAACGTTTCGAGATG 18  
|||

## RESULT 11

US-10-033-243-14  
; Sequence 14, Application US/10033243  
; Publication No. US20030049266A1  
; GENERAL INFORMATION:  
; APPLICANT: FEARON, Karen L.  
; APPLICANT: DINA, Dino  
; TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND  
; FILE REFERENCE: 377882001800  
; CURRENT APPLICATION NUMBER: US/10/033,243  
; PRIOR FILING DATE: 2002-04-03  
; PRIOR APPLICATION NUMBER: 60/258,675  
; PRIOR FILING DATE: 2000-12-27  
; NUMBER OF SEQ ID NOS: 133  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-10-033-243-14

Query Match 76.2%; Score 16; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TCGAACGTTTCGAGATG 19  
|||  
Db 3 TCGAACGTTTCGAGATG 18

## RESULT 12

US-10-176-883-139  
; Sequence 139, Application US/10176883  
; Publication No. US20030175731A1  
; GENERAL INFORMATION:  
; APPLICANT: Fearon, Karen  
; APPLICANT: Dina, Dino  
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND  
; FILE REFERENCE: 377882002000  
; CURRENT APPLICATION NUMBER: US/10/176,883  
; PRIOR FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: 60/299,883  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 60/375,253  
; PRIOR FILING DATE: 2002-04-23  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 139  
; LENGTH: 66  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-10-176-883-139

Query Match 76.2%; Score 16; DB 13; Length 66;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTTCGAGATGAT 21  
|||  
Db 8 GAACGTTTCGAGATGAT 23



RESULT 13  
US-10-177-826-139  
; Sequence 139, Application US/10177826  
; Publication No. US20030199466A1  
; GENERAL INFORMATION:  
; APPLICANT: Fearon, Karen  
; APPLICANT: Dina, Dino  
; APPLICANT: Tuck, Stephen  
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND  
; TITLE OF INVENTION: METHODS OF USING THE SAME-11  
; FILE REFERENCE: 377882002001  
; CURRENT APPLICATION NUMBER: US/10/177,826  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: 60/299,883  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 60/375,253  
; PRIOR FILING DATE: 2002-04-23  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 139  
; LENGTH: 66  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-10-177-826-139

Query Match 76.2%; Score 16; DB 13; Length 66;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 21  
|||||  
DB 8 GAACGTCGAGATGA 23

RESULT 14  
US-09-848-986-21  
; Sequence 21, Application US/09848986  
; Publication No. US20030176373A1  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Loie, Augusto F.  
; APPLICANT: Takabayashi, Kenji  
; TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and  
; TITLE OF INVENTION: Methods of Use Thereof  
; FILE REFERENCE: 06510168US1  
; CURRENT APPLICATION NUMBER: US/09/848,986  
; CURRENT FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: us 60/262321  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: us 60/202,274  
; PRIOR FILING DATE: 2000-05-05  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: ISS-ODN  
US-09-848-986-21

Query Match 71.4%; Score 15; DB 13; Length 20;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20  
|||||  
DB 6 GAACGTCGAGATGA 20

RESULT 15

US-10-233-121A-21  
; Sequence 21, Application US/10233121A  
; Publication No. US20030125284A1  
; GENERAL INFORMATION:  
; APPLICANT: RAZ, EYAL  
; APPLICANT: LOIS, AUGUSTO  
; APPLICANT: TAKABAYASHI, KENJI  
; TITLE OF INVENTION: AGENTS THAT MODULATE DNA-PK ACTIVITY AND  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: UCL-168DIV  
; CURRENT APPLICATION NUMBER: US/10/233,121A  
; CURRENT FILING DATE: 2003-03-11  
; PRIOR APPLICATION NUMBER: US 09/848,986  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: US 60/202,274  
; PRIOR FILING DATE: 2000-05-05  
; PRIOR APPLICATION NUMBER: US 60/262,321  
; PRIOR FILING DATE: 2001-01-17  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: phosphodiester or phosphorothioate oligonucleotide  
US-10-233-121A-21

Query Match 71.4%; Score 15; DB 15; Length 20;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20  
|||||  
DB 6 GAACGTCGAGATGA 20

RESULT 16  
US-09-802-686-1  
; Sequence 1, Application US/09802686  
; Patent No. US20010046967A1  
; GENERAL INFORMATION:  
; APPLICANT: Dynavax Technologies Corporation  
; APPLICANT: Van Nest, Gary  
; TITLE OF INVENTION: METHODS OF PREVENTING AND TREATING  
; TITLE OF INVENTION: RESPIRATORY VIRAL INFECTION USING IMMUNOMODULATORY  
; FILE REFERENCE: 377882000900  
; CURRENT APPLICATION NUMBER: US/09/802,686  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,583  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-686-1

Query Match 71.4%; Score 15; DB 9; Length 22;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20  
|||||  
DB 8 GAACGTCGAGATGA 22

RESULT 17  
US-09-802-686-2

```
; Sequence 2, Application US/09802686
; Patent No. US20010046967A1
; GENERAL INFORMATION:
; APPLICANT: Dynavax Technologies Corporation
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF PREVENTING AND TREATING
; TITLE OF INVENTION: RESPIRATORY VIRAL INFECTION USING IMMUNOMODULATORY
; FILE REFERENCE: 37782000900
; CURRENT APPLICATION NUMBER: US/09/802,686
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,583
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-686-2

Query Match
Best Local Similarity 71.4%; Score 15; DB 9; Length 22;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20
DB 8 GAACGTCGAGATGA 22

RESULT 18
US-09-802-685-1
; Sequence 1, Application US/09802685
; Patent No. US20020028784A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Eiden, Joseph J., Jr.
; TITLE OF INVENTION: METHODS OF PREVENTING AND TREATING VIRAL
; TITLE OF INVENTION: INFECTIONS USING IMMUNOMODULATORY POLYNUCLEOTIDE SEQUENCES
; FILE REFERENCE: 377882001600
; CURRENT APPLICATION NUMBER: US/09/802,685
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/188,302
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-685-1

Query Match
Best Local Similarity 71.4%; Score 15; DB 9; Length 22;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20
DB 8 GAACGTCGAGATGA 22

RESULT 19
US-09-802-685-2
; Sequence 2, Application US/09802685
; Patent No. US20020028784A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Eiden, Joseph J., Jr.
; TITLE OF INVENTION: METHODS OF PREVENTING AND TREATING VIRAL
```

```
; TITLE OF INVENTION: INFECTIONS USING IMMUNOMODULATORY POLYNUCLEOTIDE SEQUENCES
; FILE REFERENCE: 377882001600
; CURRENT APPLICATION NUMBER: US/09/802,685
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/188,302
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-685-2

Query Match
Best Local Similarity 71.4%; Score 15; DB 9; Length 22;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20
DB 8 GAACGTCGAGATGA 22

RESULT 20
US-09-791-500-1
; Sequence 1, Application US/09791500
; Patent No. US20020042387A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202US1
; CURRENT APPLICATION NUMBER: US/09/791,500
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
US-09-791-500-1

Query Match
Best Local Similarity 71.4%; Score 15; DB 9; Length 22;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20
DB 8 GAACGTCGAGATGA 22

RESULT 21
US-09-802-376-1
; Sequence 1, Application US/09802376
; Patent No. US20020055477A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
```

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-376-1

Query Match 71.4%; Score 15; DB 9; Length 22;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20  
|||||  
DB 8 GAACGTCGAGATGA 22

RESULT 22  
US-09-802-376-2  
; Sequence 2, Application US/09802376  
; Patent No. US20020055477A1  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; APPLICANT: Tuck, Stephen  
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF  
; FILE REFERENCE: 37788201700  
; CURRENT APPLICATION NUMBER: US/09/802,376  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,557  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-376-2

Query Match 71.4%; Score 15; DB 9; Length 22;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20  
|||||  
DB 8 GAACGTCGAGATGA 22

RESULT 23  
US-09-802-370-1  
; Sequence 1, Application US/09802370  
; Patent No. US20020098199A1  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; APPLICANT: Eiden, Joseph J. Jr.  
; TITLE OF INVENTION: METHODS OF SUPPRESSING HEPATITIS VIRUS  
; FILE REFERENCE: 377882001200  
; CURRENT APPLICATION NUMBER: US/09/802,370  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 60/188,301  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-370-1

Query Match 71.4%; Score 15; DB 9; Length 22;  
Best Local Similarity 100.0%; Pred. No. 16;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 GAACGTCGAGATGA 20  
|||||  
DB 8 GAACGTCGAGATGA 22

RESULT 24  
US-09-802-370-2  
; Sequence 2, Application US/09802370  
; Patent No. US20020098199A1  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; APPLICANT: Eiden, Joseph J. Jr.  
; TITLE OF INVENTION: METHODS OF SUPPRESSING HEPATITIS VIRUS  
; FILE REFERENCE: 377882001200  
; CURRENT APPLICATION NUMBER: US/09/802,370  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 60/188,301  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-370-2

Query Match 71.4%; Score 15; DB 9; Length 22;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20  
|||||  
DB 8 GAACGTCGAGATGA 22

RESULT 25  
US-09-802-445-1  
; Sequence 1, Application US/09802445  
; Patent No. US20020107212A1  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; APPLICANT: Eiden, Joseph J. Jr.  
; TITLE OF INVENTION: METHODS OF REDUCING PAPILLOMAVIRUS INFECTION USING IMMUNOMODULATO  
; FILE REFERENCE: 377882001300  
; CURRENT APPLICATION NUMBER: US/09/802,445  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 60/188,265  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-445-1

Query Match 71.4%; Score 15; DB 10; Length 22;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20  
|||||  
DB 8 GAACGTCGAGATGA 22

RESULT 26  
US-09-802-445-2  
; Sequence 2, Application US/09802445  
; Patent No. US20020107212A1  
; GENERAL INFORMATION:  
; APPLICANT: Van Nest, Gary  
; APPLICANT: Elden, Joseph J. Jr.  
; TITLE OF INVENTION: METHODS OF REDUCING PAPILLOMAVIRUS INFECTION USING IMMUNOMODULATORS  
; FILE REFERENCE: 377882001300  
; CURRENT APPLICATION NUMBER: US/09/802,445  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 60/188,265  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Polynucleotide containing CG  
US-09-802-445-2

Query Match 71.4%; Score 15; DB 10; Length 22;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20  
|||||  
DB 8 GAACGTTGAGATGA 22

RESULT 27  
US-09-820-484-1  
; Sequence 1, Application US/09820484  
; Patent No. US20020142977A1  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Cho, Hearn Jay  
; APPLICANT: Richman, Douglas  
; APPLICANT: Horner, Anthony A.  
; TITLE OF INVENTION: Method for Increasing a Cytotoxic T  
; TITLE OF INVENTION: Lymphocyte Response in vivo.  
; FILE REFERENCE: 06510-188US1  
; CURRENT APPLICATION NUMBER: US/09/820,484  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 60/192,537  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: US 60/203,567  
; PRIOR FILING DATE: 2000-05-11  
; PRIOR APPLICATION NUMBER: US 60/215,895  
; PRIOR FILING DATE: 2000-07-05  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN  
; NAME/KEY: modified base  
; LOCATION: (1)...(1)  
; OTHER INFORMATION: disulfide thymine  
US-09-820-484-1

Query Match 71.4%; Score 15; DB 10; Length 22;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20  
|||||  
DB 8 GAACGTTGAGATGA 22

RESULT 28  
US-09-820-484-3  
; Sequence 3, Application US/09820484  
; Patent No. US20020142977A1  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Cho, Hearn Jay  
; APPLICANT: Richman, Douglas  
; APPLICANT: Horner, Anthony A.  
; TITLE OF INVENTION: Method for Increasing a Cytotoxic T  
; TITLE OF INVENTION: Lymphocyte Response in vivo.  
; FILE REFERENCE: 06510-188US1  
; CURRENT APPLICATION NUMBER: US/09/820,484  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 60/192,537  
; PRIOR FILING DATE: 2000-03-28  
; PRIOR APPLICATION NUMBER: US 60/203,567  
; PRIOR FILING DATE: 2000-05-11  
; PRIOR APPLICATION NUMBER: US 60/215,895  
; PRIOR FILING DATE: 2000-07-05  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: phosphorothioate ISS-ODN  
US-09-820-484-3

Query Match 71.4%; Score 15; DB 10; Length 22;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20  
|||||  
DB 8 GAACGTTGAGATGA 22

RESULT 29  
US-09-828-505-1  
; Sequence 1, Application US/09828505  
; Patent No. US20020142978A1  
; GENERAL INFORMATION:  
; APPLICANT: Raz, Eyal  
; APPLICANT: Takabayashi, Kenji  
; APPLICANT: Nguyen, Minh-Duc  
; TITLE OF INVENTION: Synergistic Improvements to  
; TITLE OF INVENTION: Polynucleotide Vaccines  
; FILE REFERENCE: 6510-203  
; CURRENT APPLICATION NUMBER: US/09/828,505  
; PRIOR FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/195,890  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Immunomodulatory nucleic acid sequence  
US-09-828-505-1

Query Match 71.4%; Score 15; DB 10; Length 22;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20  
|||||  
DB 8 GAACGTTGAGATGA 22

```
RESULT 30
US-09-967-881-2
; Sequence 2, Application US/09967881
; Publication No. US20020192184A1
; GENERAL INFORMATION:
; APPLICANT: Assistance Publique - Hopitaux de Paris
; APPLICANT: Institut National de la Sante et de la Recherche M
; APPLICANT: Carpentier, Antoine
; TITLE OF INVENTION: Use of Stabilised Oligonucleotides for Preparing A Medicament wi
; TITLE OF INVENTION: Antitumor Activity
; FILE REFERENCE: 267/246 US
; CURRENT APPLICATION NUMBER: US/09/967,881
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligodeoxynucleotide
US-09-967-881-2

Query Match          71.4%; Score 15; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTTGAGATGA 20
DB      8 GAACGTTGAGATGA 22

RESULT 31
US-09-927-422A-1
; Sequence 1, Application US/09927422A
; Publication No. US20030022852A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; APPLICANT: Fearon, Karen L.
; APPLICANT: Dina, Dino
; TITLE OF INVENTION: BIODEGRADABLE IMMUNOMODULATORY
; TITLE OF INVENTION: FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37/882001420
; CURRENT APPLICATION NUMBER: US/09/927,422A
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/802,359
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/188,30
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-927-422A-1

Query Match          71.4%; Score 15; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTTGAGATGA 20
DB      8 GAACGTTGAGATGA 22

RESULT 32
US-09-927-422A-2
```

```
; Sequence 2, Application US/09927422A
; Publication No. US20030022852A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; APPLICANT: Fearon, Karen L.
; APPLICANT: Dina, Dino
; TITLE OF INVENTION: BIODEGRADABLE IMMUNOMODULATORY
; TITLE OF INVENTION: FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37/882001420
; CURRENT APPLICATION NUMBER: US/09/927,422A
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/802,359
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/188,30
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-927-422A-2

Query Match          71.4%; Score 15; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTTGAGATGA 20
DB      8 GAACGTTGAGATGA 22

RESULT 33
US-09-738-046A-3
; Sequence 3, Application US/09738046A
; Publication No. US20030054007A1
; GENERAL INFORMATION:
; APPLICANT: FELGNER, PHILIP L.
; APPLICANT: ZELPHART, OLIVIER
; TITLE OF INVENTION: INTRACELLULAR PROTEIN DELIVERY
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: GTSYS.004A
; CURRENT APPLICATION NUMBER: US/09/738,046A
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence containing Cpg sequence
US-09-738-046A-3

Query Match          71.4%; Score 15; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTTGAGATGA 20
DB      8 GAACGTTGAGATGA 22

RESULT 34
US-09-927-884-1
; Sequence 1, Application US/09927884
; Publication No. US20030059773A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
```



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; CURRENT APPLICATION NUMBER: US/09/967,464
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/236,105
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/315,905
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial sequence is synthesized
US-09-967-464-19

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAACGTCGAGATGA 20
        |||||||
Db      8 GAACGTCGAGATGA 22

RESULT 39
US-10-214-799-2
; Sequence 2, Application US/10214799
; Publication No. US20030133988A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen L. and Dina, Dino
; TITLE OF INVENTION: IMMUNOMODULATORY COMPOSITIONS,
; FILE REFERENCE: 37782003100
; CURRENT APPLICATION NUMBER: US/10/214,799
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/310,743
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/335,263
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-214-799-2

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAACGTCGAGATGA 20
        |||||||
Db      8 GAACGTCGAGATGA 22

RESULT 40
US-10-340-275-1
; Sequence 1, Application US/10340275
; Publication No. US20030143213A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Increasing a Cytotoxic T
; FILE REFERENCE: UCAL-188DIv
; CURRENT APPLICATION NUMBER: US/10/340,275
; CURRENT FILING DATE: 2003-01-10
```

```

; PRIOR APPLICATION NUMBER: 09/820,484
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
US-10-340-275-1

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAACGTCGAGATGA 20
        |||||||
Db      8 GAACGTCGAGATGA 22

RESULT 41
US-10-340-275-3
; Sequence 3, Application US/10340275
; Publication No. US20030143213A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Increasing a Cytotoxic T
; FILE REFERENCE: UCAL-188DIv
; CURRENT APPLICATION NUMBER: US/10/340,275
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 09/820,484
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: phosphorothioate ISS-ODN
US-10-340-275-3

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAACGTCGAGATGA 20
        |||||||
Db      8 GAACGTCGAGATGA 22

RESULT 42
```

```
US-10-339-885-1
; Sequence 1, Application US/10339885
; Publication No. US20030147870A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Anthony A.
; APPLICANT: Horner, Douglas
; TITLE OF INVENTION: Method for Increasing a Cytotoxic T
; TITLE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: UCAL-188CON
; CURRENT APPLICATION NUMBER: US/10/339,885
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 09/820,484
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
US-10-339-885-1
Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAACGTCGAGATGA 20
Db      8 GAACGTCGAGATGA 22

RESULT 43
US-10-339-885-3
; Sequence 3, Application US/10339885
; Publication No. US20030147870A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Increasing a Cytotoxic T
; TITLE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: UCAL-188CON
; CURRENT APPLICATION NUMBER: US/10/339,885
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 09/820,484
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
```

```
; OTHER INFORMATION: phosphorothioate ISS-ODN
US-10-339-885-3
Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAACGTCGAGATGA 20
Db      8 GAACGTCGAGATGA 22

RESULT 44
US-09-848-986-1
; Sequence 1, Application US/09848986
; Publication No. US20030176373A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Lois, Augusto F.
; APPLICANT: Takabayashi, Kenji
; TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and
; TITLE OF INVENTION: Methods of Use Thereof
; FILE REFERENCE: 06510168US1
; CURRENT APPLICATION NUMBER: US/09/848,986
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: us 60/262321
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: us 60/202,274
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ISS-ODN
US-09-848-986-1
Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAACGTCGAGATGA 20
Db      8 GAACGTCGAGATGA 22

RESULT 45
US-10-176-883-2
; Sequence 2, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-I
; FILE REFERENCE: 377882002000
; CURRENT APPLICATION NUMBER: US/10/176,883
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
```



US-10-176-883-2

Query Match 71.4%; Score 15; DB 13; Length 22;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
|||||  
DB 8 GAACGTCGAGATGA 22

RESULT 46

US-10-176-883-24  
; Sequence 24, Application US/10176883  
; Publication No. US20030175731A1  
; GENERAL INFORMATION:

APPLICANT: Fearon, Karen  
APPLICANT: Dina, Dino  
TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND  
TITLE OF INVENTION: METHODS OF USING THE SAME-I  
FILE REFERENCE: 377882002000  
CURRENT FILING DATE: 2002-06-21  
PRIOR APPLICATION NUMBER: 60/299,883  
PRIOR FILING DATE: 2001-06-21  
PRIOR APPLICATION NUMBER: 60/375,253  
PRIOR FILING DATE: 2002-04-23  
NUMBER OF SEQ ID NOS: 141  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 24  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic construct  
US-10-176-883-24

Query Match 71.4%; Score 15; DB 13; Length 22;  
Best Local Similarity 93.3%; Pred. No. 16;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
|||||  
DB 8 GAACGTCGAGATGA 22

RESULT 47

US-10-176-883-34  
; Sequence 34, Application US/10176883  
; Publication No. US20030175731A1  
; GENERAL INFORMATION:

APPLICANT: Fearon, Karen  
APPLICANT: Dina, Dino  
TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND  
TITLE OF INVENTION: METHODS OF USING THE SAME-I  
FILE REFERENCE: 377882002000  
CURRENT FILING DATE: 2002-06-21  
PRIOR APPLICATION NUMBER: 60/299,883  
PRIOR FILING DATE: 2001-06-21  
PRIOR APPLICATION NUMBER: 60/375,253  
PRIOR FILING DATE: 2002-04-23  
NUMBER OF SEQ ID NOS: 141  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 34  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic construct  
US-10-176-883-34

Query Match 71.4%; Score 15; DB 13; Length 22;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20  
|||||  
DB 8 GAACGTCGAGATGA 22

RESULT 48

US-10-176-883-44  
; Sequence 44, Application US/10176883  
; Publication No. US20030175731A1  
; GENERAL INFORMATION:

APPLICANT: Fearon, Karen  
APPLICANT: Dina, Dino  
TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND  
TITLE OF INVENTION: METHODS OF USING THE SAME-I  
FILE REFERENCE: 377882002000  
CURRENT FILING DATE: 2002-06-21  
PRIOR APPLICATION NUMBER: 60/299,883  
PRIOR FILING DATE: 2001-06-21  
PRIOR APPLICATION NUMBER: 60/375,253  
PRIOR FILING DATE: 2002-04-23  
NUMBER OF SEQ ID NOS: 141  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 44  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic construct  
US-10-176-883-44

Query Match 71.4%; Score 15; DB 13; Length 22;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCGTCGAACGTTGCA 15  
|||||  
DB 1 TCGTCGAACGTTGCA 15

RESULT 49

US-10-176-883-79  
; Sequence 79, Application US/10176883  
; Publication No. US20030175731A1  
; GENERAL INFORMATION:

APPLICANT: Fearon, Karen  
APPLICANT: Dina, Dino  
TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND  
TITLE OF INVENTION: METHODS OF USING THE SAME-I  
FILE REFERENCE: 377882002000  
CURRENT FILING DATE: 2002-06-21  
PRIOR APPLICATION NUMBER: 60/299,883  
PRIOR FILING DATE: 2001-06-21  
PRIOR APPLICATION NUMBER: 60/375,253  
PRIOR FILING DATE: 2002-04-23  
NUMBER OF SEQ ID NOS: 141  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 79  
LENGTH: 22  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic construct  
US-10-176-883-79

Query Match 71.4%; Score 15; DB 13; Length 22;  
Best Local Similarity 93.3%; Pred. No. 16;  
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20  
|||||  
DB 8 GAACGTTGAGATGA 22

RESULT 50

US-10-176-883-84  
; Sequence 84, Application US/10176883  
; Publication No. US20030175731A1  
; GENERAL INFORMATION:  
; APPLICANT: Fearon, Karen  
; APPLICANT: Dina, Dino

; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND  
; FILE REFERENCE: 377882002000  
; CURRENT APPLICATION NUMBER: US/10/176,883  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: 60/299,883  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 60/375,253  
; PRIOR FILING DATE: 2002-04-23  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 84  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
; NAME/KEY: variation  
; LOCATION: 2, 5  
; OTHER INFORMATION: n = 5-bromocytosine  
US-10-176-883-84

Query Match 71.4%; Score 15; DB 13; Length 22;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20  
|||||  
DB 8 GAACGTTGAGATGA 22

RESULT 51

US-10-176-883-85  
; Sequence 85, Application US/10176883  
; Publication No. US20030175731A1  
; GENERAL INFORMATION:  
; APPLICANT: Fearon, Karen  
; APPLICANT: Dina, Dino  
; APPLICANT: Tuck, Stephen  
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND  
; FILE REFERENCE: 377882002000  
; CURRENT APPLICATION NUMBER: US/10/176,883  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: 60/299,883  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 60/375,253  
; PRIOR FILING DATE: 2002-04-23  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 85  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-10-176-883-85

; OTHER INFORMATION: Synthetic construct  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: 5  
; OTHER INFORMATION: n = 5-bromocytosine  
US-10-176-883-85

Query Match 71.4%; Score 15; DB 13; Length 22;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20  
|||||  
DB 8 GAACGTTGAGATGA 22

RESULT 52

US-10-176-883-134  
; Sequence 134, Application US/10176883  
; Publication No. US20030175731A1  
; GENERAL INFORMATION:  
; APPLICANT: Fearon, Karen  
; APPLICANT: Dina, Dino

; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND  
; FILE REFERENCE: 377882002000  
; CURRENT APPLICATION NUMBER: US/10/176,883  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: 60/299,883  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 60/375,253  
; PRIOR FILING DATE: 2002-04-23  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 134  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-10-176-883-134

Query Match 71.4%; Score 15; DB 13; Length 22;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20  
|||||  
DB 8 GAACGTTGAGATGA 22

RESULT 53

US-10-176-883-140  
; Sequence 140, Application US/10176883  
; Publication No. US20030175731A1  
; GENERAL INFORMATION:  
; APPLICANT: Fearon, Karen  
; APPLICANT: Dina, Dino  
; APPLICANT: Tuck, Stephen  
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND  
; FILE REFERENCE: 377882002000  
; CURRENT APPLICATION NUMBER: US/10/176,883  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: 60/299,883  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 60/375,253  
; PRIOR FILING DATE: 2002-04-23  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 140  
; LENGTH: 22

US-10-176-883-84  
; Sequence 84, Application US/10176883  
; Publication No. US20030175731A1  
; GENERAL INFORMATION:  
; APPLICANT: Fearon, Karen  
; APPLICANT: Dina, Dino  
; APPLICANT: Tuck, Stephen  
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND  
; FILE REFERENCE: 377882002000  
; CURRENT APPLICATION NUMBER: US/10/176,883  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: 60/299,883  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 60/375,253  
; PRIOR FILING DATE: 2002-04-23  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 84  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-10-176-883-84

US-10-176-883-140  
; Sequence 140, Application US/10176883  
; Publication No. US20030175731A1  
; GENERAL INFORMATION:  
; APPLICANT: Fearon, Karen  
; APPLICANT: Dina, Dino  
; APPLICANT: Tuck, Stephen  
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND  
; FILE REFERENCE: 377882002000  
; CURRENT APPLICATION NUMBER: US/10/176,883  
; CURRENT FILING DATE: 2002-06-21  
; PRIOR APPLICATION NUMBER: 60/299,883  
; PRIOR FILING DATE: 2001-06-21  
; PRIOR APPLICATION NUMBER: 60/375,253  
; PRIOR FILING DATE: 2002-04-23  
; NUMBER OF SEQ ID NOS: 141  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 140  
; LENGTH: 22

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: n = thymine attached to a reactive linking group
US-10-176-883-140
```

```

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 GAACGTCGAGATGA 20
        |||
        8 GAACGTCGAGATGA 22
```

## RESULT 54

```

US-10-176-883-141
; Sequence 141, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; FILE REFERENCE: 37782002000
; CURRENT APPLICATION NUMBER: US/10/176,883
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: n = thymine attached to a reactive linking group
US-10-176-883-141
```

```

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 GAACGTCGAGATGA 20
        |||
        8 GAACGTCGAGATGA 22
```

## RESULT 55

```

US-10-412-151-1
; Sequence 1, Application US/10412151
; Publication No. US20030176389A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; FILE REFERENCE: UCAL-202CON
; CURRENT APPLICATION NUMBER: US/10/412,151
; PRIOR FILING DATE: 2003-04-11
; CURRENT APPLICATION NUMBER: 09/791,500
; PRIOR FILING DATE: 2001-02-22
```

```

; PRIOR APPLICATION NUMBER: 60/184,256
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
; OTHER INFORMATION: oligonucleotide primer
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-10-412-151-1
```

```

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 GAACGTCGAGATGA 20
        |||
        8 GAACGTCGAGATGA 22
```

## RESULT 56

```

US-10-177-826-2
; Sequence 2, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; FILE REFERENCE: 37782002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-177-826-2
```

```

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 GAACGTCGAGATGA 20
        |||
        8 GAACGTCGAGATGA 22
```

## RESULT 57

```

US-10-177-826-24
; Sequence 24, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; FILE REFERENCE: 37782002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; PRIOR FILING DATE: 2002-06-21
```

```

; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-177-826-24

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 93.3%; Pred. No. 16;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTTGAGATGA 20
        |||||:|||||
        8 GAACGTTGAGATGA 22

RESULT 58
US-10-177-826-34
; Sequence 34, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-II
; FILE REFERENCE: 37782002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-177-826-34

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTTGAGATGA 20
        |||||:|||||
        8 GAACGTTGAGATGA 22

RESULT 59
US-10-177-826-44
; Sequence 44, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-II
; FILE REFERENCE: 37782002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
```

```

; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-177-826-44

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCGTGAACGTTGCA 15
        |||||:|||||
        1 TCGTGAACGTTGCA 15

RESULT 60
US-10-177-826-79
; Sequence 79, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-II
; FILE REFERENCE: 37782002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-177-826-79

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 93.3%; Pred. No. 16;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTTGAGATGA 20
        |||||:|||||
        8 GAACGTTGAGATGA 22

RESULT 61
US-10-177-826-84
; Sequence 84, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-II
; FILE REFERENCE: 37782002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
```

```
/ PRIOR APPLICATION NUMBER: 60/375,253
/ PRIOR FILING DATE: 2002-04-23
/ NUMBER OF SEQ ID NOS: 141
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 84
/ LENGTH: 22
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic construct
/ NAME/KEY: variation
/ LOCATION: 2, 5
/ OTHER INFORMATION: n = 5-bromocytosine
US-10-177-826-84

Query Match      71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAACGTCGAGATGA 20
Db      8 GAACGTCGAGATGA 22

RESULT 62
US-10-177-826-85
/ Sequence 85, Application US/10177826
/ Publication No. US20030199466A1
/ GENERAL INFORMATION:
/ APPLICANT: Fearon, Karen
/ APPLICANT: Dina, Dino
/ APPLICANT: Tuck, Stephen
/ TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
/ TITLE OF INVENTION: METHODS OF USING THE SAME-II
/ FILE REFERENCE: 377882002001
/ CURRENT APPLICATION NUMBER: US/10/177,826
/ CURRENT FILING DATE: 2002-06-21
/ PRIOR APPLICATION NUMBER: 60/299,883
/ PRIOR FILING DATE: 2001-06-21
/ PRIOR APPLICATION NUMBER: 60/375,253
/ PRIOR FILING DATE: 2002-04-23
/ NUMBER OF SEQ ID NOS: 141
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 85
/ LENGTH: 22
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic construct
/ NAME/KEY: variation
/ LOCATION: 5
/ OTHER INFORMATION: n = 5-bromocytosine
US-10-177-826-85

Query Match      71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAACGTCGAGATGA 20
Db      8 GAACGTCGAGATGA 22

RESULT 63
US-10-177-826-134
/ Sequence 134, Application US/10177826
/ Publication No. US20030199466A1
/ GENERAL INFORMATION:
/ APPLICANT: Fearon, Karen
/ APPLICANT: Dina, Dino
/ APPLICANT: Tuck, Stephen
```

```
/ TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
/ TITLE OF INVENTION: METHODS OF USING THE SAME-II
/ FILE REFERENCE: 377882002001
/ CURRENT APPLICATION NUMBER: US/10/177,826
/ CURRENT FILING DATE: 2002-06-21
/ PRIOR APPLICATION NUMBER: 60/299,883
/ PRIOR FILING DATE: 2001-06-21
/ PRIOR APPLICATION NUMBER: 60/375,253
/ PRIOR FILING DATE: 2002-04-23
/ NUMBER OF SEQ ID NOS: 141
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 134
/ LENGTH: 22
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic construct
US-10-177-826-134

Query Match      71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAACGTCGAGATGA 20
Db      8 GAACGTCGAGATGA 22

RESULT 64
US-10-177-826-140
/ Sequence 140, Application US/10177826
/ Publication No. US20030199466A1
/ GENERAL INFORMATION:
/ APPLICANT: Fearon, Karen
/ APPLICANT: Dina, Dino
/ APPLICANT: Tuck, Stephen
/ TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
/ TITLE OF INVENTION: METHODS OF USING THE SAME-II
/ FILE REFERENCE: 377882002001
/ CURRENT APPLICATION NUMBER: US/10/177,826
/ CURRENT FILING DATE: 2002-06-21
/ PRIOR APPLICATION NUMBER: 60/299,883
/ PRIOR FILING DATE: 2001-06-21
/ PRIOR APPLICATION NUMBER: 60/375,253
/ PRIOR FILING DATE: 2002-04-23
/ NUMBER OF SEQ ID NOS: 141
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 140
/ LENGTH: 22
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic construct
/ NAME/KEY: modified_base
/ LOCATION: 1
/ OTHER INFORMATION: n = thymine attached to a reactive linking group
US-10-177-826-140

Query Match      71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAACGTCGAGATGA 20
Db      8 GAACGTCGAGATGA 22

RESULT 65
US-10-177-826-141
/ Sequence 141, Application US/10177826
/ Publication No. US20030199466A1
/ GENERAL INFORMATION:
```

```
; APPLICANT: Fearon, Karen
; APPLICANT: Tina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; FILE REFERENCE: 377882002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: n = thymine attached to a reactive linking group
US-10-177-826-141

Query Match
Best Local Similarity 71.4%; Score 15; DB 13; Length 22;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
Db      6 GAACGTTGCAGATGA 20
      8 GAACGTTGCAGATGA 22

RESULT 66
US-10-357-760-1
; Sequence 1, Application US/10357760
; Publication No. US20030216340A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Eiden, Joseph J. Jr.
; TITLE OF INVENTION: METHODS OF SUPPRESSING HEPATITIS VIRUS
; FILE REFERENCE: 377882001200
; CURRENT APPLICATION NUMBER: US/10/357,760
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/802,370
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/188,301
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-10-357-760-1

Query Match
Best Local Similarity 71.4%; Score 15; DB 13; Length 22;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
Db      6 GAACGTTGCAGATGA 20
      8 GAACGTTGCAGATGA 22

RESULT 67
US-10-357-760-2
; Sequence 2, Application US/10357760
```

```
; Publication No. US20030216340A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Eiden, Joseph J. Jr.
; TITLE OF INVENTION: METHODS OF SUPPRESSING HEPATITIS VIRUS
; FILE REFERENCE: 377882001200
; CURRENT APPLICATION NUMBER: US/10/357,760
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/802,370
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/188,301
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-10-357-760-2

Query Match
Best Local Similarity 71.4%; Score 15; DB 13; Length 22;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
Db      6 GAACGTTGCAGATGA 20
      8 GAACGTTGCAGATGA 22

RESULT 68
US-10-056-420-4
; Sequence 4, Application US/10056420
; Publication No. US2003004428A1
; GENERAL INFORMATION:
; APPLICANT: Moss, Ronald B.
; APPLICANT: Carlo, Dennis J.
; TITLE OF INVENTION: Method For Treating an HIV-Infected
; TITLE OF INVENTION: Individual By Combining Immunization With Structured
; FILE REFERENCE: P-1M 5158
; CURRENT APPLICATION NUMBER: US/10/056,420
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/264,476
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: exemplary ISS sequence
US-10-056-420-4

Query Match
Best Local Similarity 71.4%; Score 15; DB 15; Length 22;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
Db      6 GAACGTTGCAGATGA 20
      8 GAACGTTGCAGATGA 22

RESULT 69
US-10-033-243-2
; Sequence 2, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
; APPLICANT: FEARON, Karen L.
; APPLICANT: DINA, Dino
```

```

; TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
; FILE REFERENCE: 37782001800
; CURRENT APPLICATION NUMBER: US/10/033,243
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/258,675
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-2

Query Match      71.4% Score 15; DB 15; Length 22;
Best Local Similarity 93.3%; Pred. No. 16;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTCGAGATGA 20
DB      8 GAACGTCGAGATGA 22

RESULT 70
US-10-033-243-12
; Sequence 12, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
; APPLICANT: FEARON, Karen L.
; APPLICANT: DINA, Dino
; TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
; FILE REFERENCE: 37782001800
; CURRENT APPLICATION NUMBER: US/10/033,243
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/258,675
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-12

Query Match      71.4% Score 15; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTCGAGATGA 20
DB      8 GAACGTCGAGATGA 22

RESULT 71
US-10-033-243-22
; Sequence 22, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
; APPLICANT: FEARON, Karen L.
; APPLICANT: DINA, Dino
; TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
; FILE REFERENCE: 37782001800
; CURRENT APPLICATION NUMBER: US/10/033,243
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/258,675
; PRIOR FILING DATE: 2000-12-27
```

```

; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-22

Query Match      71.4% Score 15; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCGTGAACGTTGCA 15
DB      1 TCGTGAACGTTGCA 15

RESULT 72
US-10-033-243-40
; Sequence 40, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
; APPLICANT: FEARON, Karen L.
; APPLICANT: DINA, Dino
; TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
; FILE REFERENCE: 37782001800
; CURRENT APPLICATION NUMBER: US/10/033,243
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/258,675
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-40

Query Match      71.4% Score 15; DB 15; Length 22;
Best Local Similarity 93.3%; Pred. No. 16;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTCGAGATGA 20
DB      8 GAACGTCGAGATGA 22

RESULT 73
US-10-033-243-45
; Sequence 45, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
; APPLICANT: FEARON, Karen L.
; APPLICANT: DINA, Dino
; TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
; FILE REFERENCE: 37782001800
; CURRENT APPLICATION NUMBER: US/10/033,243
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/258,675
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
OTHER INFORMATION: Polynucleotide containing CG
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2..5
OTHER INFORMATION: n = 5-bromocytosine
US-10-033-243-45
```

```
Query Match          71.4%; Score 15; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 GAACGTTGAGATGA 20
         |||||
Db       8 GAACGTTGAGATGA 22
```

```
RESULT 74
US-10-033-243-46
; Sequence 46, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
; APPLICANT: FEARON, Karen L.
; APPLICANT: DINA, Dino
; TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; FILE REFERENCE: 37782001800
; CURRENT APPLICATION NUMBER: US/10/033,243
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/258,675
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 5
; OTHER INFORMATION: n = 5-bromocytosine
US-10-033-243-46
```

```
Query Match          71.4%; Score 15; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 GAACGTTGAGATGA 20
         |||||
Db       8 GAACGTTGAGATGA 22
```

```
RESULT 75
US-10-033-243-59
; Sequence 59, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
; APPLICANT: FEARON, Karen L.
; APPLICANT: DINA, Dino
; TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; FILE REFERENCE: 37782001800
; CURRENT APPLICATION NUMBER: US/10/033,243
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/258,675
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
FEATURE:
OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-59
```

```
Query Match          71.4%; Score 15; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 GAACGTTGAGATGA 20
         |||||
Db       8 GAACGTTGAGATGA 22
```

```
Search completed: December 17, 2003, 11:06:43
Job time : 1153 secs
```



Wed Dec 17 13:16:37 2003

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 17, 2003, 09:15:24 : Search time 47 Seconds  
(without alignments)  
197.214 Million cell updates/sec

Title: US-10-033-243-132

Perfect score: 21

Sequence: 1 tcgcgcgaactcgcgatgatc 21

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : Issued Patents NA:\*

1: /cgn2\_6/ptodata/1/1na/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/1/1na/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/1na/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/1na/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/1na/PCTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/1na/backfiles1.seq:\*Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	71.4	22	4	US-09-235-742-19
2	15	71.4	22	4	US-09-347-343-32
3	15	71.4	22	4	US-09-820-484-1
4	15	71.4	22	4	US-09-820-484-3
5	15	71.4	22	4	US-09-774-403A-1
6	15	66.7	816	3	US-08-776-251-10
7	14	66.7	816	3	US-08-776-251-10
8	14	66.7	4403765	3	US-09-103-840A-2
9	14	66.7	4411529	3	US-09-103-840A-1
10	13	61.9	321	3	US-09-060-756-260
11	13	61.9	321	3	US-09-240-274-197
12	13	61.9	321	4	US-09-670-314-260
13	13	61.9	462	4	US-09-252-991A-16046
14	13	61.9	573	4	US-09-252-991A-9162
15	13	61.9	663	4	US-09-252-991A-9246
16	13	61.9	762	4	US-09-252-991A-16554
17	13	61.9	813	4	US-09-107-530A-1566
18	13	61.9	1221	4	US-09-252-991A-8921
19	13	61.9	1461	4	US-09-252-991A-9074
20	13	61.9	1545	4	US-09-252-991A-8710
21	13	61.9	1986	4	US-09-252-991A-16138
22	13	61.9	2091	4	US-09-252-991A-15954
23	13	61.9	43804	4	US-09-171-461-1
24	12	57.1	20	4	US-09-286-098-11
25	12	57.1	20	4	US-09-325-193A-91
26	12	57.1	22	2	US-08-882-704A-18
27	12	57.1	22	2	US-08-882-704A-18

28	12	57.1	22	4	US-09-151-957-18	Sequence 18, Appl
29	12	57.1	22	4	US-09-151-957-18	Sequence 18, Appl
30	12	57.1	22	4	US-08-633-768A-12	Sequence 12, Appl
31	12	57.1	77	3	US-08-399-412A-58	Sequence 58, Appl
32	12	57.1	160	3	US-08-633-768A-14	Sequence 14, Appl
33	12	57.1	186	3	US-09-328-352-3855	Sequence 3855, Ap
34	12	57.1	212	4	US-09-313-294A-2448	Sequence 2448, Ap
35	12	57.1	268	4	US-09-313-294A-2857	Sequence 2857, Ap
36	12	57.1	283	4	US-09-313-294A-4896	Sequence 4896, Ap
37	12	57.1	288	4	US-09-252-991A-69	Sequence 69, Appl
38	12	57.1	378	4	US-09-252-991A-5259	Sequence 5259, Ap
39	12	57.1	406	3	US-09-060-756-563	Sequence 563, App
40	12	57.1	406	3	US-09-670-314-563	Sequence 563, App
41	12	57.1	432	4	US-09-252-991A-3530	Sequence 3530, Ap
42	12	57.1	441	4	US-09-252-991A-4565	Sequence 4565, Ap
43	12	57.1	658	3	US-08-861-774E-69	Sequence 69, Appl
44	12	57.1	813	4	US-09-198-119C-78	Sequence 78, Appl
45	12	57.1	830	4	US-09-107-532A-1566	Sequence 1566, Ap
46	12	57.1	830	4	US-09-198-119C-84	Sequence 84, Appl
47	12	57.1	906	4	US-09-252-991A-5994	Sequence 5994, Ap
48	12	57.1	981	4	US-09-252-991A-5231	Sequence 5231, Ap
49	12	57.1	1002	4	US-09-252-991A-3539	Sequence 3539, Ap
50	12	57.1	1009	4	US-09-091-097-37	Sequence 37, Appl
51	12	57.1	1038	4	US-09-252-991A-16116	Sequence 16116, A
52	12	57.1	1038	4	US-09-252-991A-16487	Sequence 16487, A
53	12	57.1	1113	1	US-08-229-287-1	Sequence 1, Appl
54	12	57.1	1119	4	US-09-252-991A-6391	Sequence 6391, Ap
55	12	57.1	1303	2	US-08-793-410-11	Sequence 11, Appl
56	12	57.1	1362	4	US-09-328-352-943	Sequence 943, App
57	12	57.1	1368	4	US-09-252-991A-64	Sequence 64, Appl
58	12	57.1	1443	4	US-09-252-991A-6308	Sequence 6308, Ap
59	12	57.1	1578	4	US-09-351-224E-7	Sequence 7, Appl
60	12	57.1	1578	4	US-09-677-682B-7	Sequence 7, Appl
61	12	57.1	1578	4	US-09-677-682B-7	Sequence 7, Appl
62	12	57.1	1644	4	US-09-252-991A-3548	Sequence 3548, Ap
63	12	57.1	1764	4	US-09-351-224E-6	Sequence 6, Appl
64	12	57.1	1764	4	US-09-677-682B-6	Sequence 6, Appl
65	12	57.1	1764	4	US-09-677-682B-6	Sequence 6, Appl
66	12	57.1	1836	4	US-07-754-918A-1	Sequence 1, Appl
67	12	57.1	1900	1	US-09-555-000-1	Sequence 1, Appl
68	12	57.1	2058	1	US-08-358-117-1	Sequence 1, Appl
69	12	57.1	2058	3	US-08-470-588-1	Sequence 1, Appl
70	12	57.1	2426	3	US-08-528-026C-3	Sequence 3, Appl
71	12	57.1	2595	4	US-09-221-017B-225	Sequence 225, App
72	12	57.1	2760	4	US-09-619-353-13	Sequence 13, Appl
73	12	57.1	2832	4	US-09-221-017B-462	Sequence 462, App
74	12	57.1	2854	4	US-09-252-991A-3523	Sequence 3523, Ap
75	12	57.1	3664	4	US-08-936-165A-66	Sequence 66, Appl
76	12	57.1	3664	4	US-07-880-913-1	Sequence 1, Appl
77	12	57.1	3872	5	PCT-US93-12169-1	Sequence 1, Appl
78	12	57.1	5648	3	US-09-371-008-1	Sequence 1, Appl
79	12	57.1	6909	4	US-09-199-637A-111	Sequence 11, App
80	12	57.1	7527	4	US-09-252-991A-71	Sequence 71, Appl
81	12	57.1	12566	4	US-08-961-527-149	Sequence 149, App
82	12	57.1	13825	4	US-09-634-238-29	Sequence 29, Appl
83	12	57.1	35412	4	US-08-311-731A-132	Sequence 132, App
84	12	57.1	71989	4	US-09-443-501A-2	Sequence 2, Appl
85	12	57.1	536165	4	US-09-214-808-1	Sequence 1, Appl
86	12	57.1	1830121	4	US-09-557-884-1	Sequence 1, Appl
87	12	57.1	1830121	4	US-09-557-884-1	Sequence 1, Appl
88	12	57.1	1830121	4	US-09-643-990A-1	Sequence 1, Appl
89	12	57.1	1830121	4	US-09-643-990A-1	Sequence 1, Appl
90	12	57.1	4413765	3	US-09-103-840A-1	Sequence 1, Appl
91	12	57.1	4413765	3	US-09-103-840A-1	Sequence 1, Appl
92	11	52.4	21	4	US-09-374-168-62	Sequence 62, Appl
93	11	52.4	22	4	US-09-797-403A-2	Sequence 2, Appl
94	11	52.4	24	1	US-08-064-271-9	Sequence 9, Appl
95	11	52.4	24	3	US-08-930-589A-9	Sequence 9, Appl
96	11	52.4	24	3	US-09-599-781-9	Sequence 9, Appl
97	11	52.4	26	4	US-09-322-409-153	Sequence 153, App
98	11	52.4	26	4	US-09-451-527-153	Sequence 153, App
99	11	52.4	39	1	US-08-293-892-1	Sequence 1, Appl
100	11	52.4	39	1	US-08-459-892-1	Sequence 1, Appl



Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTTGAGATGA 20  
Db 8 GAACGTTGAGATGA 22

## RESULT 5

US-09-774-403A-1  
; Sequence 1, Application US/09774403A  
; Patent No. 6552006  
; GENERAL INFORMATION:  
; APPLICANT: Eval Raz  
; APPLICANT: Richard Kornbluth  
; APPLICANT: Antonio Catanzaro  
; APPLICANT: Tomoko Hayashi  
; APPLICANT: Dennis Carson  
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in  
; TITLE OF INVENTION: Treatment of Infection by an Intracellular Pathogen  
; FILE REFERENCE: UCA1166  
; CURRENT APPLICATION NUMBER: US/09/774,403A  
; CURRENT FILING DATE: 2002-04-15  
; PRIOR APPLICATION NUMBER: 60/179,353  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Immunomodulatory sequence  
US-09-774-403A-1

Query Match 71.4%; Score 15; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTTGAGATGA 20  
Db 8 GAACGTTGAGATGA 22

## RESULT 6

US-08-776-251-10  
; Sequence 10, Application US/08776251  
; Patent No. 6025340  
; GENERAL INFORMATION:  
; APPLICANT: Springer, Caroline J  
; APPLICANT: Marais, Richard  
; TITLE OF INVENTION: Surface expression of enzyme in gene directed prodrug therapy  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon & Vanderhye  
; STREET: 1100 No. 6025340th Glebe Road, 8th Floor  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: USA  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/776,251  
; FILING DATE: 31-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB95/01782  
; FILING DATE: 27-JUL-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9415167.7  
; FILING DATE: 27-JUL-1994

ATTORNEY/AGENT INFORMATION:  
; NAME: Arthur R. Crawford  
; REGISTRATION NUMBER: 25,327  
; REFERENCE/DOCKET NUMBER: 620-20  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 816 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-08-776-251-10

## US-08-776-251-10

Query Match 66.7%; Score 14; DB 3; Length 816;  
Best Local Similarity 100.0%; Pred. No. 6.5;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCGAACGTTGAGA 17  
Db 619 TCGAACGTTGAGA 632

## RESULT 7

US-08-776-251-10/c  
; Sequence 10, Application US/08776251  
; Patent No. 6025340  
; GENERAL INFORMATION:  
; APPLICANT: Springer, Caroline J  
; APPLICANT: Marais, Richard  
; TITLE OF INVENTION: Surface expression of enzyme in gene directed prodrug therapy  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon & Vanderhye  
; STREET: 1100 No. 6025340th Glebe Road, 8th Floor  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: USA  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/776,251  
; FILING DATE: 31-JAN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB95/01782  
; FILING DATE: 27-JUL-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9415167.7  
; FILING DATE: 27-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arthur R. Crawford  
; REGISTRATION NUMBER: 25,327  
; REFERENCE/DOCKET NUMBER: 620-20  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 816 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
US-08-776-251-10

Query Match 66.7%; Score 14; DB 3; Length 816;  
Best Local Similarity 100.0%; Pred. No. 6.5;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCGAACGTTGAGA 17  
Db 801 TCGAACGTTGAGA 788

```
RESULT 8
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match          66.7%; Score 14; DB 3; Length 4403765;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCGTGAACGTTG 14
        |||||
DB       735047 TCGTGAACGTTG 735034

RESULT 9
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match          66.7%; Score 14; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCGTGAACGTTG 14
        |||||
DB       733615 TCGTGAACGTTG 733602

RESULT 10
US-09-060-756-260
; Sequence 260, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
```

```
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/060,756
; CURRENT FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 260
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (various positions within the sequence)
; OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-060-756-260

Query Match          61.9%; Score 13; DB 3; Length 321;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 ACGTTCGAGATGA 20
        |||||
DB       75 ACGTTCGAGATGA 87

RESULT 11
US-09-240-274-197/c
; Sequence 197, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THERMOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 197
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH8
US-09-240-274-197

Query Match          61.9%; Score 13; DB 3; Length 321;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CGAAGTTGAGA 17
        |||||
DB       292 CGAAGTTGAGA 280

RESULT 12
US-09-670-314-260
; Sequence 260, Application US/09670314
; Patent No. 6492506
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
```

;; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM  
;; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA  
;; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA  
;; FILE REFERENCE: 3495-0169  
;; CURRENT APPLICATION NUMBER: US/09/670,314  
;; PRIOR FILING DATE: 2001-01-12  
;; PRIOR APPLICATION NUMBER: 09/060,756  
;; PRIOR FILING DATE: 1998-04-16  
;; NUMBER OF SEQ ID NOS: 743  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 260  
;; LENGTH: 321  
;; TYPE: DNA  
;; ORGANISM: Mycobacterium tuberculosis  
;; FEATURE:  
;; NAME/KEY: unsure  
;; LOCATION: (various positions within the sequence)  
;; OTHER INFORMATION: applicants are uncertain of bases designated as "n"  
US-09-670-314-260

Query Match 61.9%; Score 13; DB 4; Length 321;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACCTTCGAGATCA 20  
Db 75 ACCTTCGAGATCA 87

RESULT 13  
US-09-252-991A-16046  
;; Sequence 16046, Application US/09252991A  
;; Patent No. 6551795  
;; GENERAL INFORMATION:  
;; APPLICANT: Marc J. Rubenfield et al.  
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
;; TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
;; FILE REFERENCE: 107196.136  
;; CURRENT APPLICATION NUMBER: US/09/252,991A  
;; CURRENT FILING DATE: 1999-02-18  
;; PRIOR APPLICATION NUMBER: US 60/074,788  
;; PRIOR FILING DATE: 1998-02-18  
;; PRIOR APPLICATION NUMBER: US 60/094,190  
;; PRIOR FILING DATE: 1998-07-27  
;; NUMBER OF SEQ ID NOS: 33142  
;; SEQ ID NO 16046  
;; LENGTH: 462  
;; TYPE: DNA  
;; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-16046

Query Match 61.9%; Score 13; DB 4; Length 462;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACCTTCGAGATCA 20  
Db 34 ACCTTCGAGATCA 46

RESULT 14  
US-09-252-991A-9162/c  
;; Sequence 9162, Application US/09252991A  
;; Patent No. 6551795  
;; GENERAL INFORMATION:  
;; APPLICANT: Marc J. Rubenfield et al.  
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
;; TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
;; FILE REFERENCE: 107196.136  
;; CURRENT APPLICATION NUMBER: US/09/252,991A  
;; CURRENT FILING DATE: 1999-02-18  
;; PRIOR APPLICATION NUMBER: US 60/074,788  
;; PRIOR FILING DATE: 1998-02-18

;; PRIOR APPLICATION NUMBER: US 60/094,190  
;; PRIOR FILING DATE: 1998-07-27  
;; NUMBER OF SEQ ID NOS: 33142  
;; SEQ ID NO 9162  
;; LENGTH: 573  
;; TYPE: DNA  
;; ORGANISM: Pseudomonas aeruginosa  
;; FEATURE:  
;; NAME/KEY: unsure  
;; LOCATION: (17)  
;; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.  
US-09-252-991A-9162

Query Match 61.9%; Score 13; DB 4; Length 573;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTCGAGAT 18  
Db 286 GAACGTCGAGAT 274

RESULT 15  
US-09-252-991A-9246/c  
;; Sequence 9246, Application US/09252991A  
;; Patent No. 6551795  
;; GENERAL INFORMATION:  
;; APPLICANT: Marc J. Rubenfield et al.  
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
;; TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
;; FILE REFERENCE: 107196.136  
;; CURRENT APPLICATION NUMBER: US/09/252,991A  
;; CURRENT FILING DATE: 1999-02-18  
;; PRIOR APPLICATION NUMBER: US 60/074,788  
;; PRIOR FILING DATE: 1998-02-18  
;; PRIOR APPLICATION NUMBER: US 60/094,190  
;; PRIOR FILING DATE: 1998-07-27  
;; NUMBER OF SEQ ID NOS: 33142  
;; SEQ ID NO 9246  
;; LENGTH: 663  
;; TYPE: DNA  
;; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9246

Query Match 61.9%; Score 13; DB 4; Length 663;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTCGAGAT 18  
Db 45 GAACGTCGAGAT 33

RESULT 16  
US-09-252-991A-16554/c  
;; Sequence 16554, Application US/09252991A  
;; Patent No. 6551795  
;; GENERAL INFORMATION:  
;; APPLICANT: Marc J. Rubenfield et al.  
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
;; TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
;; FILE REFERENCE: 107196.136  
;; CURRENT APPLICATION NUMBER: US/09/252,991A  
;; CURRENT FILING DATE: 1999-02-18  
;; PRIOR APPLICATION NUMBER: US 60/074,788  
;; PRIOR FILING DATE: 1998-02-18  
;; PRIOR APPLICATION NUMBER: US 60/094,190  
;; PRIOR FILING DATE: 1998-07-27  
;; NUMBER OF SEQ ID NOS: 33142  
;; SEQ ID NO 16554  
;; LENGTH: 762  
;; TYPE: DNA  
;; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-16554

Query Match 61.9%; Score 13; DB 4; Length 762;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ACCTTCGAGATGA 20  
|||||  
DB 555 ACCTTCGAGATGA 543

RESULT 17

US-09-107-532A-1566  
; Sequence 1566, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts

COUNTRY: USA  
ZIP: 02354

COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571  
FILING DATE: JULY 2, 1997

ATTORNEY/AGENT INFORMATION:  
NAME: Atinello, Pamela Deneka  
REGISTRATION NUMBER: 40,489

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-8277  
TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 1566:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 813 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: (8) LOCATION 1...813

SEQUENCE DESCRIPTION: SEQ ID NO: 1566:  
US-09-107-532A-1566

Query Match 61.9%; Score 13; DB 4; Length 813;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTGGAACGTTGCA 15  
|||||  
DB 241 GTGGAACGTTGCA 253

RESULT 18  
US-09-252-991A-8921  
; Sequence 8921, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 8921  
LENGTH: 1221  
TYPE: DNA

ORGANISM: Pseudomonas aeruginosa  
FEATURE:  
NAME/KEY: unsure

LOCATION: (458)  
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.

US-09-252-991A-8921

Query Match 61.9%; Score 13; DB 4; Length 1221;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGAT 18  
|||||  
DB 189 GAACGTCGAGAT 201

RESULT 19

US-09-252-991A-9074/C  
; Sequence 9074, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 9074  
LENGTH: 1461  
TYPE: DNA

ORGANISM: Pseudomonas aeruginosa  
FEATURE:  
NAME/KEY: unsure

LOCATION: (951),(1078)  
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.

US-09-252-991A-9074

Query Match 61.9%; Score 13; DB 4; Length 1461;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGAT 18  
|||||  
DB 212 GAACGTCGAGAT 200

RESULT 20  
US-09-252-991A-8710  
; Sequence 8710, Application US/09252991A

```
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8710
; LENGTH: 1545
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (760)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-8710
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Query Match      61.9%; Score 13; DB 4; Length 1545;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      6 GACGCTCGAGAT 18
      |||||
Db      491 GACGCTCGAGAT 503
```

## RESULT 21

```
US-09-252-991A-16328/c
; Sequence 16328, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16328
; LENGTH: 1986
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16328
```

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Query Match      61.9%; Score 13; DB 4; Length 1986;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      8 ACGTTCGAGATGA 20
      |||||
Db      1676 ACGTTCGAGATGA 1664
```

## RESULT 22

```
US-09-252-991A-15954
; Sequence 15954, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
```

```
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15954
; LENGTH: 2091
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15954
```

```
Query Match      61.9%; Score 13; DB 4; Length 2091;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      8 ACGTTCGAGATGA 20
      |||||
Db      473 ACGTTCGAGATGA 485
```

## RESULT 23

```
US-09-171-461-1
; Sequence 1, Application US/09171461
; Patent No. 6335016
; GENERAL INFORMATION:
; APPLICANT: Baker, Adam
; APPLICANT: Cotten, Matthew
; APPLICANT: Chiodera, Susanna
; APPLICANT: Kuzbauer, Robert
; APPLICANT: Schaffner, Gotthold
; TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) Virus
; FILE REFERENCE: 0652.1800000
; CURRENT APPLICATION NUMBER: US/09/171,461
; CURRENT FILING DATE: 1999-01-12
; EARLIER APPLICATION NUMBER: PCT/EP97/01944
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 43804
; TYPE: DNA
; ORGANISM: CELO Virus
```

```
; FEATURE:
; NAME/KEY: gene
; LOCATION: (12193)..(15043)
; OTHER INFORMATION: /gene: L1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15080)
; OTHER INFORMATION: /note= L2 region penton base splice acceptor site
; FEATURE:
; NAME/KEY: gene
; LOCATION: (15110)..(17495)
; OTHER INFORMATION: /gene: L2
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: (17526)
; FEATURE:
; NAME/KEY: gene
; LOCATION: (17559)..(21754)
; OTHER INFORMATION: /gene: L3
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (18261)
; OTHER INFORMATION: /gene: L3 /note= hexon splice acceptor site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (21102)
; OTHER INFORMATION: /gene: L3 /note= protease splice acceptor site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (21123)
```

```
OTHER INFORMATION: /gene: l3 /note= protease splice acceptor site
FEATURE:
NAME/KEY: polyA site
LOCATION: (21767)
FEATURE:
NAME/KEY: polyA site
LOCATION: (21824)
FEATURE:
NAME/KEY: polyA site
LOCATION: (21835)
FEATURE:
NAME/KEY: polyA site
LOCATION: (21882)
FEATURE:
NAME/KEY: misc feature
LOCATION: (23608)
OTHER INFORMATION: /note= 100k splice acceptor site
FEATURE:
NAME/KEY: misc feature
LOCATION: (23649)
OTHER INFORMATION: /note= 100k splice acceptor site
FEATURE:
NAME/KEY: gene
LOCATION: (23680)..(27886)
OTHER INFORMATION: /gene: L4
FEATURE:
NAME/KEY: polyA site
LOCATION: (27920)
FEATURE:
NAME/KEY: misc feature
LOCATION: (28315)
OTHER INFORMATION: /note= fibre splice acceptor site
FEATURE:
NAME/KEY: misc feature
LOCATION: (28311)
OTHER INFORMATION: / note= fibre splice acceptor site
FEATURE:
NAME/KEY: gene
LOCATION: (28363)..(31768)
OTHER INFORMATION: /gene: L5
FEATURE:
NAME/KEY: misc feature
LOCATION: (30511)
OTHER INFORMATION: /gene: L5
FEATURE:
NAME/KEY: polyA site
LOCATION: (31770)
US-09-171-461-1

Query Match          61.9%; Score 13; DB 4; Length 43804;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTCGAGAT 18
      |||||
Db      25862 GAACGTCGAGAT 25874

RESULT 24
US-09-286-098-11/c
; Sequence 11, Application US/09286098
; GENERAL INFORMATION:
; APPLICANT: Kriegl, Arthur M.
; TITLE OF INVENTION: Methods and Products for Stimulating the
; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/286,098
; EARLIER FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,729
; EARLIER FILING DATE: 1998-04-03
```

```
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-286-098-11

Query Match          57.1%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTCGAGA 17
      |||||
Db      18 GAACGTCGAGA 7

RESULT 25
US-09-325-193A-91/c
; Sequence 91, Application US/09325193A
; Patent No. 6406705
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Schorr, Joachim
; APPLICANT: Kriegl, Arthur M.
; TITLE OF INVENTION: Use of Nucleic Acids Containing
; TITLE OF INVENTION: Unmethylated CpG Dinucleotide as an Adjuvant
; FILE REFERENCE: C1039/7025/HCL
; CURRENT APPLICATION NUMBER: US/09/325,193A
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: US 09/154,614
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: PCT/US98/04703
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: US 60/040,376
; PRIOR FILING DATE: 1997-03-10
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 91
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-09-325-193A-91

Query Match          57.1%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTCGAGA 17
      |||||
Db      18 GAACGTCGAGA 7

RESULT 26
US-08-882-704A-18
; Sequence 18, Application US/08882704A
; Patent No. 5879906
; GENERAL INFORMATION:
; APPLICANT: Jefferson, Richard A.
; APPLICANT: Wilson, Katherine J.
; APPLICANT: Leader, Michael
; TITLE OF INVENTION: GLUCURONIDE REPRESSORS AND USES THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6100 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
```



ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/882,704A  
FILING DATE: 25-JUN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5879906tendburg Ph.D., Carol  
REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 190106.404  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 622-6031  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-882-704A-18

Query Match 57.1%; Score 12; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCGAACGTTGCA 15  
|||||  
Db 8 TCGAACGTTGCA 19

RESULT 27  
US-08-882-704A-18/c  
Sequence 18, Application US/08882704A  
Patent No. 5879906  
GENERAL INFORMATION:  
APPLICANT: Jefferson, Richard A.  
APPLICANT: Wilson, Katherine J.  
APPLICANT: Leader, Michael  
TITLE OF INVENTION: GLUCURONIDE REPRESSORS AND USES THEREOF  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/882,704A  
FILING DATE: 25-JUN-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5879906tendburg Ph.D., Carol  
REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 190106.404  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 622-6031  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-882-704A-18

Query Match 57.1%; Score 12; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCGAACGTTGCA 15  
|||||  
Db 19 TCGAACGTTGCA 8

RESULT 28  
US-09-151-957-18  
Sequence 18, Application US/09151957  
Patent No. 6429292  
GENERAL INFORMATION:  
APPLICANT: Jefferson, Richard A.  
APPLICANT: Wilson, Katherine J.  
APPLICANT: Leader, Michael  
TITLE OF INVENTION: GLUCURONIDE REPRESSORS AND USES THEREOF  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/151,957  
FILING DATE: 11-SEP-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/882,704  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6429292tendburg Ph.D., Carol  
REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 190106.404  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 622-6031  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-151-957-18

Query Match 57.1%; Score 12; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCGAACGTTGCA 15  
|||||  
Db 8 TCGAACGTTGCA 19

RESULT 29  
US-09-151-957-18/c  
Sequence 18, Application US/09151957  
Patent No. 6429292  
GENERAL INFORMATION:  
APPLICANT: Jefferson, Richard A.  
APPLICANT: Wilson, Katherine J.  
APPLICANT: Leader, Michael

TITLE OF INVENTION: GLUCURONIDE REPRESSORS AND USES THEREOF  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESS: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/151,957  
FILING DATE: 11-Sep-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/882,704  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6429292lenburg Ph.D., Carol  
REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 190106.404  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-151-957-18

Query Match 57.1%; Score 12; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCGAAGCTCGA 15  
DB 19 TCGAAGCTCGA 8

RESULT 30  
US-08-633-768A-12/c  
Sequence 12, Application US/08633768A  
GENERAL INFORMATION:  
PATENT No. 6013504  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/399,412A  
FILING DATE: 6-MARCH-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 536  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Julie L. Bernard  
REGISTRATION NUMBER: 36,450  
REFERENCE/DOCKET NUMBER: NEX27

APPLICATION NUMBER: US/08/633,768A  
FILING DATE: 02-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9321301.5  
FILING DATE: 15-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: DY0U7.001APC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714-760-0404  
TELEFAX: 714-760-9502  
TELEX:  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 71 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
US-08-633-768A-12

Query Match 57.1%; Score 12; DB 3; Length 71;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGCTTCGAG 16  
DB 26 CGAAGCTTCGAG 15

RESULT 31  
US-08-399-412A-58/c  
Sequence 58, Application US/08399412A  
PATENT No. 5622828  
GENERAL INFORMATION:  
APPLICANT: Palma, David  
TITLE OF INVENTION: High-Affinity Oligonucleotide  
TITLE OF INVENTION: Ligands to Secretory Phospholipase  
TITLE OF INVENTION: A2 (sPLA2)  
NUMBER OF SEQUENCES: 122  
CORRESPONDENCE ADDRESS:  
ADDRESS: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/399,412A  
FILING DATE: 6-MARCH-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/714,131  
FILING DATE: 10-JUNE-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 536  
FILING DATE: 11-JUNE-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/964,624  
FILING DATE: 21-OCTOBER-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Julie L. Bernard  
REGISTRATION NUMBER: 36,450  
REFERENCE/DOCKET NUMBER: NEX27

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 77 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-399-412A-58

Query Match 57.1%; Score 12; DB 1; Length 77;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTCGAAGCTTCG 14  
|||||  
DB 59 GTCGAAGCTTCG 48

RESULT 32  
US-08-633-768A-14/c  
Sequence 14, Application US/08633768A  
Patent No. 6013504  
GENERAL INFORMATION:  
APPLICANT: YU, SHUKUN  
BOUSSEN, KIRSTEN  
APPLICANT: KRAGH, KARSTEN  
APPLICANT: BOJKO, MAJIA  
APPLICANT: NIELSEN, JOHN  
APPLICANT: MARCUSSEN, JAN  
TITLE OF INVENTION: ALPHA-1-4-GLUCAN LYASE FROM  
TITLE OF INVENTION: A FUNGUS INFECTED ALGAE, ITS PURIFICATION  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Knobbe, Martens, Olson & Bear  
STREET: 620 Newport Center Drive 16th Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FaecesQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/633,768A  
FILING DATE: 02-JUL-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9321301.5  
FILING DATE: 15-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Altman, Daniel E  
REGISTRATION NUMBER: 34,115  
REFERENCE/DOCKET NUMBER: DYOU7.001APC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 714-760-0404  
TELEFAX: 714-760-9502  
TELEX:  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 160 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
US-08-633-768A-14  
Query Match 57.1%; Score 12; DB 3; Length 160;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGCTTCGAG 16  
|||||  
DB 26 CGAAGCTTCGAG 15

RESULT 33  
US-09-328-352-3855/c  
Sequence 3855, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 3855  
LENGTH: 186  
TYPE: DNA  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-3855

Query Match 57.1%; Score 12; DB 4; Length 186;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCGAGATGAT 21  
|||||  
DB 98 GTTCGAGATGAT 87

RESULT 34  
US-09-313-294A-2448  
Sequence 2448, Application US/09313294A  
Patent No. 6476212  
GENERAL INFORMATION:  
APPLICANT: Lalgudi, Raghunath V.  
APPLICANT: Ito, Laura Y.  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
FILE REFERENCE: PL-0017 US  
CURRENT APPLICATION NUMBER: US/09/313,294A  
CURRENT FILING DATE: 1999-05-14  
NUMBER OF SEQ ID NOS: 7600  
SOFTWARE: PERL Program  
SEQ ID NO 2448  
LENGTH: 212  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. 6476212 700552684H1  
US-09-313-294A-2448

Query Match 57.1%; Score 12; DB 4; Length 212;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCGAGATGAT 21  
|||||  
DB 9 GTTCGAGATGAT 20

RESULT 35  
US-09-313-284A-2857  
Sequence 2857, Application US/09313284A  
Patent No. 6476212  
GENERAL INFORMATION:  
APPLICANT: Lalgudi, Raghunath V.  
APPLICANT: Ito, Laura Y.  
APPLICANT: Sherman, Bradley K.

```

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 2857
; LENGTH: 268
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700553386H1
; NAME/KEY: unsure
; LOCATION: 257
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-2857

Query Match          57.1%; Score 12; DB 4; Length 268;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 GTTCGAGATGAT 21
Db      132 GTTCGAGATGAT 143

RESULT 36
US-09-313-294A-4896/C
; Sequence 4896, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalguadi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 4896
; LENGTH: 283
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700349228H1
; NAME/KEY: unsure
; LOCATION: 122, 140
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-4896

Query Match          57.1%; Score 12; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTCGAGA 17
Db      100 GAACGTCGAGA 89

RESULT 37
US-09-252-991A-69
; Sequence 69, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
```

```

; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 69
; LENGTH: 288
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-69

Query Match          57.1%; Score 12; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CGAACGTCGAG 16
Db      83 CGAACGTCGAG 94

RESULT 38
US-09-252-991A-5259/C
; Sequence 5259, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5259
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5259

Query Match          57.1%; Score 12; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GTCGAACGTCG 14
Db      27 GTCGAACGTCG 16

RESULT 39
US-09-060-756-563
; Sequence 563, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/060,756
; CURRENT FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 563
; LENGTH: 406
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
```

NAME/KEY: unsure  
LOCATION: (various positions within the sequence)  
OTHER INFORMATION: applicants are uncertain of bases designated as "n"  
US-09-060-756-563

Query Match 57.1%; Score 12; DB 3; Length 406;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTGGAACGTTG 14  
|||||  
DB 287 GTGGAACGTTG 298

RESULT 40  
US-09-670-314-563  
Sequence 563, Application US/09670314  
Patent No. 6492506  
GENERAL INFORMATION:  
APPLICANT: Cole, Stewart  
APPLICANT: Buchrieser-Brosch, Roland  
APPLICANT: Gordon, Stephen  
APPLICANT: Billault, Alain  
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM  
TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA  
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA  
FILE REFERENCE: 3495-0169  
CURRENT APPLICATION NUMBER: US/09/670,314  
CURRENT FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: 09/060,756  
PRIOR FILING DATE: 1998-04-16  
NUMBER OF SEQ ID NOS: 743  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 563  
LENGTH: 406  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (various positions within the sequence)  
OTHER INFORMATION: applicants are uncertain of bases designated as "n"  
US-09-670-314-563

Query Match 57.1%; Score 12; DB 4; Length 406;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTGGAACGTTG 14  
|||||  
DB 287 GTGGAACGTTG 298

RESULT 41  
US-09-252-991A-3530  
Sequence 3530, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 3530  
LENGTH: 432  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-3530

Query Match 57.1%; Score 12; DB 4; Length 432;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGTTCGAGATGA 20  
|||||  
DB 421 CGTTCGAGATGA 432

RESULT 42  
US-09-252-991A-4565  
Sequence 4565, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 4565  
LENGTH: 441  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-4565

Query Match 57.1%; Score 12; DB 4; Length 441;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCGAGATGAT 21  
|||||  
DB 55 GTTCGAGATGAT 66

RESULT 43  
US-08-861-774E-69/C  
Sequence 69, Application US/08861774E  
Patent No. 6287007  
GENERAL INFORMATION:  
APPLICANT: Waters, Barbara  
APPLICANT: Miao, Yiyuan  
APPLICANT: Ho, Yap  
APPLICANT: Tong, Seow  
TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR  
TITLE OF INVENTION: BIOACTIVE MOLECULES  
FILE REFERENCE: 9993-006  
CURRENT APPLICATION NUMBER: US/08/861,774E  
CURRENT FILING DATE: 1997-05-22  
NUMBER OF SEQ ID NOS: 94  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 69  
LENGTH: 658  
TYPE: DNA  
ORGANISM: Unesa florida  
US-08-861-774E-69

Query Match 57.1%; Score 12; DB 3; Length 658;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCGAGATGAT 21  
|||||  
DB 187 GTTCGAGATGAT 176

RESULT 44

US-09-198-119C-78  
; Sequence 78, Application US/09198119C  
; Patent No. 6417428  
; GENERAL INFORMATION:  
; APPLICANT: Thomasow, Michael  
; APPLICANT: Stockinger, Eric  
; APPLICANT: Jaglo-Otosen, Kirsten  
; APPLICANT: Gilmour, Sarah  
; APPLICANT: Zarka, Daniel  
; APPLICANT: Jiang, Cai-zhong  
; TITLE OF INVENTION: Plant Having Altered Environmental Stress Tolerance  
; FILE REFERENCE: 19117.713 Seq List  
; CURRENT APPLICATION NUMBER: US/09/198,119C  
; PRIOR FILING DATE: 1998-11-23  
; PRIOR APPLICATION NUMBER: US 08/706,270  
; PRIOR FILING DATE: 1998-09-04  
; PRIOR APPLICATION NUMBER: US 09/018,233  
; PRIOR FILING DATE: 1998-02-03  
; PRIOR APPLICATION NUMBER: US 09/017,816  
; PRIOR FILING DATE: 1998-02-03  
; PRIOR APPLICATION NUMBER: US 09/018,235  
; PRIOR FILING DATE: 1998-02-03  
; PRIOR APPLICATION NUMBER: US 09/017,575  
; PRIOR FILING DATE: 1998-02-03  
; PRIOR APPLICATION NUMBER: US 09/018,227  
; PRIOR FILING DATE: 1998-02-03  
; PRIOR APPLICATION NUMBER: US 09/018,234  
; PRIOR FILING DATE: 1998-02-03  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 78  
; LENGTH: 806  
; TYPE: DNA  
; ORGANISM: Brassica rapa  
; FEATURE:  
; OTHER INFORMATION: brcBF3 gene  
; US-09-198-119C-78

Query Match 57.1%; Score 12; DB 4; Length 806;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACCTTCGAGATG 19  
|||||  
Db 692 ACCTTCGAGATG 703

RESULT 45  
US-09-107-532A-1566/C  
; Sequence 1566, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ariniello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 1566:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 813 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...813  
SEQUENCE DESCRIPTION: SEQ ID NO: 1566:  
US-09-107-532A-1566

Query Match 57.1%; Score 12; DB 4; Length 813;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCGAACGTTGCA 15  
|||||  
Db 253 TCGAACGTTGCA 242

RESULT 46  
US-09-198-119C-84  
; Sequence 84, Application US/09198119C  
; Patent No. 6417428  
; GENERAL INFORMATION:  
; APPLICANT: Thomasow, Michael  
; APPLICANT: Stockinger, Eric  
; APPLICANT: Jaglo-Otosen, Kirsten  
; APPLICANT: Gilmour, Sarah  
; APPLICANT: Zarka, Daniel  
; APPLICANT: Jiang, Cai-zhong  
; TITLE OF INVENTION: Plant Having Altered Environmental Stress Tolerance  
; FILE REFERENCE: 19117.713 Seq List  
; CURRENT APPLICATION NUMBER: US/09/198,119C  
; PRIOR FILING DATE: 1998-11-23  
; PRIOR APPLICATION NUMBER: US 08/706,270  
; PRIOR FILING DATE: 1998-09-04  
; PRIOR APPLICATION NUMBER: US 09/018,233  
; PRIOR FILING DATE: 1998-02-03  
; PRIOR APPLICATION NUMBER: US 09/017,816  
; PRIOR FILING DATE: 1998-02-03  
; PRIOR APPLICATION NUMBER: US 09/018,235  
; PRIOR FILING DATE: 1998-02-03  
; PRIOR APPLICATION NUMBER: US 09/017,575  
; PRIOR FILING DATE: 1998-02-03  
; PRIOR APPLICATION NUMBER: US 09/018,227  
; PRIOR FILING DATE: 1998-02-03  
; PRIOR APPLICATION NUMBER: US 09/018,234  
; PRIOR FILING DATE: 1998-02-03  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 84  
; LENGTH: 830  
; TYPE: DNA  
; ORGANISM: Brassica rapa  
; FEATURE:  
; OTHER INFORMATION: brcBF6 gene

US-09-198-119C-84

## Query Match

Best Local Similarity 57.1%; Score 12; DB 4; Length 830;  
Matches 12; Conservativity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;

QY 8 ACCTCGAGATG 19

DB 696 ACCTCGAGATG 707

## RESULT 47

US-09-252-991A-5994

Sequence 5994, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 5994

LENGTH: 906

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-5994

## Query Match

Best Local Similarity 57.1%; Score 12; DB 4; Length 906;  
Matches 12; Conservativity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;

QY 10 GTTCGAGATGAT 21

DB 237 GTTCGAGATGAT 248

## RESULT 48

US-09-252-991A-5231/C

Sequence 5231, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 5231

LENGTH: 981

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-5231

## Query Match

Best Local Similarity 57.1%; Score 12; DB 4; Length 981;  
Matches 12; Conservativity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;

QY 3 GTCGAAGCTTCG 14

DB 22 GTCGAAGCTTCG 11

## RESULT 49

US-09-252-991A-3539

Sequence 3539, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 3539

LENGTH: 1002

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-3539

## Query Match

Best Local Similarity 57.1%; Score 12; DB 4; Length 1002;  
Matches 12; Conservativity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;

QY 9 CGTTCGAGATGA 20

DB 717 CGTTCGAGATGA 728

## RESULT 50

US-09-091-097-37/C

Sequence 37, Application US/09091097

Patent No. 6432407

GENERAL INFORMATION:

APPLICANT: TAKESAKO, KAZUTOH

APPLICANT: OKADO, TAKASHI

APPLICANT: YAGIHARA, TOMOKO

APPLICANT: KURODA, MASANOBU

APPLICANT: ONISHI, YOSHIMI

APPLICANT: KATO, IKUNOSHIN

APPLICANT: AKIYAMA, KAZUO

APPLICANT: YASUEDA, HIROSHI

APPLICANT: YAMAGUCHI, HIROYO

TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

STREET: BIRCH, STEWART, KOLASCH &amp; BIRCH, LLP

CITY: PO BOX 747

STATE: VA

COUNTRY: USA

ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/091,097

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: WEINER, MARC S.

REGISTRATION NUMBER: 32,181

REFERENCE/DOCKET NUMBER: 1422-0346P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-205-8050

TELEFAX: 703-205-8050

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 1009 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
US-09-091-097-37

Query Match 57.1%; Score 12; DB 4; Length 1009;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCGAGATGAT 21  
|||||  
Db 306 GTTCGAGATGAT 295

RESULT 51  
US-09-252-991A-16116/c  
Sequence 16116, Application US/09252991A  
Patent No. 6551795

GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 16116  
LENGTH: 1038  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-16116

Query Match 57.1%; Score 12; DB 4; Length 1038;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGTTCGAGATGA 20  
|||||  
Db 920 CGTTCGAGATGA 909

RESULT 52  
US-09-252-991A-16487  
Sequence 16487, Application US/09252991A  
Patent No. 6551795

GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 16487  
LENGTH: 1038  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-16487

Query Match 57.1%; Score 12; DB 4; Length 1038;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGTTCGAGATGA 20  
|||||  
Db 374 CGTTCGAGATGA 385

RESULT 53  
US-08-229-287-1/c

Sequence 1, Application US/08229287  
Patent No. 5530193  
GENERAL INFORMATION:  
APPLICANT: Clark Jr., John M.  
APPLICANT: Jilka, Joseph M.  
APPLICANT: Murry, Lynn E.  
APPLICANT: Scarafia, Liliana E.  
TITLE OF INVENTION: VIRUS RESISTANT CORN PLANTS  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sandoz Agro, Inc.  
STREET: 975 California Avenue  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/229,287  
FILING DATE:

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/067,257  
FILING DATE: 25-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/817,922  
FILING DATE: 08-JAN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Marcus-Wyner, Lynn  
REGISTRATION NUMBER: 34,869  
REFERENCE/DOCKET NUMBER: 135-1084/XCC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/354-3588  
TELEFAX: 415/857-1125

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1113 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:

NAME/KEY: CDS  
LOCATION: 1..876  
US-08-229-287-1

Query Match 57.1%; Score 12; DB 1; Length 1113;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCGAGATGAT 21  
|||||  
Db 695 GTTCGAGATGAT 684

RESULT 54  
US-09-252-991A-6391/c  
Sequence 6391, Application US/09252991A  
Patent No. 6551795

GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
PRIOR FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 16487  
LENGTH: 1038  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-16487



FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 6391  
LENGTH: 1119  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-6391

Query Match  
Best Local Similarity 100.0%; Score 12; DB 4; Length 1119;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCGAGATGAT 21  
|||||  
DB 1095 GTTCGAGATGAT 1084

RESULT 55  
US-08-793-410-11/c  
Sequence 11, Application US/08793410  
Patent No. 5955650

GENERAL INFORMATION:  
APPLICANT: HITZ, WILLIAM DEAN  
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF CANOLA  
TITLE OF INVENTION: AND SOYBEAN PALMITOYL-ACP THIO-  
TITLE OF INVENTION: ESTERASE GENES AND THEIR USE IN  
TITLE OF INVENTION: THE REGULATION OF FATTY ACID  
TITLE OF INVENTION: AND CANOLA PLANTS  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY  
STREET: 1007 MARKET STREET  
CITY: WILMINGTON  
STATE: DELAWARE  
COUNTRY: USA  
ZIP: 19898

COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.50 INCH  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MICROSOFT WINDOWS 95  
SOFTWARE: MICROSOFT WORD VERSION 7.0A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,410  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/10627  
FILING DATE: AUGUST 25, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CHRISTENBURY, LYNN M.  
REGISTRATION NUMBER: 30,971  
REFERENCE/DOCKET NUMBER: CR-9567-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 302-992-5481  
TELEFAX: 302-773-0164  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1303 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
US-08-793-410-11

Query Match  
Best Local Similarity 100.0%; Score 12; DB 2; Length 1303;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AACGTTGAGAT 18  
|||||  
DB 23 AACGTTGAGAT 12

RESULT 56  
US-09-328-352-943  
Sequence 943, Application US/09328352  
Patent No. 6562958

GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 943  
LENGTH: 1362  
TYPE: DNA  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-943

Query Match  
Best Local Similarity 100.0%; Score 12; DB 4; Length 1362;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCGAGATGAT 21  
|||||  
DB 949 GTTCGAGATGAT 960

RESULT 57  
US-09-252-991A-64  
Sequence 64, Application US/09252991A  
Patent No. 6551795

GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 64  
LENGTH: 1368  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-64

Query Match  
Best Local Similarity 100.0%; Score 12; DB 4; Length 1368;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGTTGAG 16  
|||||  
DB 928 CGAAGTTGAG 939

RESULT 58  
US-09-252-991A-6308/c  
Sequence 6308, Application US/09252991A  
Patent No. 6551795

GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.

;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
;; TITLE OF INVENTION: AERUDINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
;; FILE REFERENCE: 107196.136  
;; CURRENT APPLICATION NUMBER: US/09/252,991A  
;; PRIOR FILING DATE: 1999-02-18  
;; PRIOR APPLICATION NUMBER: US 60/074,788  
;; PRIOR FILING DATE: 1998-02-18  
;; PRIOR APPLICATION NUMBER: US 60/094,190  
;; PRIOR FILING DATE: 1998-07-27  
;; NUMBER OF SEQ ID NOS: 33142  
;; SEQ ID NO: 6308  
;; LENGTH: 1443  
;; TYPE: DNA  
;; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-6308

Query Match 57.1%; Score 12; DB 4; Length 1443;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGTTCGAGATGAT 21  
|||  
Db 994 GTTCGAGATGAT 983

RESULT 59  
US-09-351-224E-7/c  
; Sequence 7, Application US/09351224E  
; Patent No. 6388171  
; GENERAL INFORMATION:  
; APPLICANT: Duvick, Jon  
; APPLICANT: Maddox, Joyce  
; APPLICANT: Gilliam, Jacob  
; APPLICANT: Folkerts, Otto  
; APPLICANT: Crasta, Oswald R.  
; TITLE OF INVENTION: Compositions and Methods for Fumonisin  
; FILE REFERENCE: 5718-111  
; CURRENT APPLICATION NUMBER: US/09/351,224E  
; CURRENT FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 1578  
; TYPE: DNA  
; ORGANISM: Exophiala spinifera  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: permease, fully spliced cDNA  
US-09-351-224E-7

Query Match 57.1%; Score 12; DB 4; Length 1578;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGTTCGAGATGA 20  
|||  
Db 1109 CGTTCGAGATGA 1098

RESULT 60  
US-09-677-488A-7/c  
; Sequence 7, Application US/09677488A  
; Patent No. 6482621  
; GENERAL INFORMATION:  
; APPLICANT: Duvick, Jon  
; APPLICANT: Maddox, Joyce  
; APPLICANT: Gilliam, Jacob  
; APPLICANT: Folkerts, Otto  
; APPLICANT: Crasta, Oswald R.  
; TITLE OF INVENTION: Compositions and Methods for Fumonisin  
; FILE REFERENCE: 107196.136

;; FILE REFERENCE: 35718/204100  
;; CURRENT APPLICATION NUMBER: US/09/677,488A  
;; CURRENT FILING DATE: 2000-10-02  
;; PRIOR APPLICATION NUMBER: 09/351,224  
;; PRIOR FILING DATE: 1999-07-12  
;; NUMBER OF SEQ ID NOS: 11  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO: 7  
;; LENGTH: 1578  
;; TYPE: DNA  
;; ORGANISM: Exophiala spinifera  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: permease, fully spliced cDNA  
US-09-677-488A-7

Query Match 57.1%; Score 12; DB 4; Length 1578;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGTTCGAGATGA 20  
|||  
Db 1109 CGTTCGAGATGA 1098

RESULT 61  
US-09-677-682B-7/c  
; Sequence 7, Application US/09677682B  
; Patent No. 6534291  
; GENERAL INFORMATION:  
; APPLICANT: Duvick, Jon  
; APPLICANT: Maddox, Joyce  
; APPLICANT: Gilliam, Jacob  
; APPLICANT: Folkerts, Otto  
; APPLICANT: Crasta, Oswald R.  
; TITLE OF INVENTION: Compositions and Methods for Fumonisin  
; FILE REFERENCE: 35718/204101  
; CURRENT APPLICATION NUMBER: US/09/677,682B  
; CURRENT FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 09/351,224  
; PRIOR FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 1578  
; TYPE: DNA  
; ORGANISM: Exophiala spinifera  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: permease, fully spliced cDNA  
US-09-677-682B-7

Query Match 57.1%; Score 12; DB 4; Length 1578;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGTTCGAGATGA 20  
|||  
Db 1109 CGTTCGAGATGA 1098

RESULT 62  
US-09-252-991A-354E/c  
; Sequence 3548, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136

```
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ CURRENT FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 3548
/ LENGTH: 1644
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3548
```

```
Query Match          57.1%; Score 12; DB 4; Length 1644;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      9 CGTTCGAGATGA 20
        |||||
        380 CGTTCGAGATGA 369
```

```
RESULT 63
US-09-351-224E-6/c
/ Sequence 6, Application US/09351224E
/ Patent No. 6388171
/ GENERAL INFORMATION:
/ APPLICANT: Duvick, Jon
/ APPLICANT: Maddox, Joyce
/ APPLICANT: Gilliam, Jacob
/ APPLICANT: Folkerts, Otto
/ APPLICANT: Craeta, Oswald R.
/ TITLE OF INVENTION: Compositions and Methods for Fumonisin
/ TITLE OF INVENTION: Detoxification
/ FILE REFERENCE: 5718-111
/ CURRENT APPLICATION NUMBER: US/09/351,224E
/ CURRENT FILING DATE: 1999-07-12
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 1764
/ TYPE: DNA
/ ORGANISM: Exophiala spinifera
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: permealase, partially spliced cDNA
US-09-351-224E-6
```

```
Query Match          57.1%; Score 12; DB 4; Length 1764;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      9 CGTTCGAGATGA 20
        |||||
        1113 CGTTCGAGATGA 1102
```

```
RESULT 64
US-09-677-488A-6/c
/ Sequence 6, Application US/09677488A
/ Patent No. 6482621
/ GENERAL INFORMATION:
/ APPLICANT: Duvick, Jon
/ APPLICANT: Maddox, Joyce
/ APPLICANT: Gilliam, Jacob
/ APPLICANT: Folkerts, Otto
/ APPLICANT: Craeta, Oswald R.
/ TITLE OF INVENTION: Compositions and Methods for Fumonisin
/ TITLE OF INVENTION: Detoxification
/ FILE REFERENCE: 35718/204100
/ CURRENT APPLICATION NUMBER: US/09/677,488A
/ CURRENT FILING DATE: 2000-10-02
```

```
/ PRIOR APPLICATION NUMBER: 09/351,224
/ PRIOR FILING DATE: 1999-07-12
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 1764
/ TYPE: DNA
/ ORGANISM: Exophiala spinifera
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: permealase, partially spliced cDNA
US-09-677-488A-6
```

```
Query Match          57.1%; Score 12; DB 4; Length 1764;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      9 CGTTCGAGATGA 20
        |||||
        1113 CGTTCGAGATGA 1102
```

```
RESULT 65
US-09-677-682B-6/c
/ Sequence 6, Application US/09677682B
/ Patent No. 6534291
/ GENERAL INFORMATION:
/ APPLICANT: Duvick, Jon
/ APPLICANT: Maddox, Joyce
/ APPLICANT: Gilliam, Jacob
/ APPLICANT: Folkerts, Otto
/ APPLICANT: Craeta, Oswald R.
/ TITLE OF INVENTION: Compositions and Methods for Fumonisin
/ TITLE OF INVENTION: Detoxification
/ FILE REFERENCE: 35718/204101
/ CURRENT APPLICATION NUMBER: US/09/677,682B
/ CURRENT FILING DATE: 2000-10-02
/ PRIOR APPLICATION NUMBER: 09/351,224
/ PRIOR FILING DATE: 1999-07-12
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 1764
/ TYPE: DNA
/ ORGANISM: Exophiala spinifera
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: permealase, partially spliced cDNA
US-09-677-682B-6
```

```
Query Match          57.1%; Score 12; DB 4; Length 1764;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      9 CGTTCGAGATGA 20
        |||||
        1113 CGTTCGAGATGA 1102
```

```
RESULT 66
US-07-754-918A-1
/ Sequence 1, Application US/07754918A
/ Patent No. 5286484
/ GENERAL INFORMATION:
/ APPLICANT: Rodriguez, R.S. et al
/ TITLE OF INVENTION: NICKING SITE SEQUENCE CODING FOR AN
/ TITLE OF INVENTION: OUTER MEMBRANE PROTEIN FROM NEISSERIA MENINGITIDIS AND USE
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Stanger, Michaelson, Spivak and Wallace, Bsq.
```

STREET: Parkway 109 Office Center, 328 Newman Springs  
STREET: Road, P. O. Box 8489  
CITY: Red Bank  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07701

## COMPUTER READABLE FORM:

MEDIUM TYPE: 5 1/4" 360KB IBM compatible diskette  
COMPUTER: IBM PS/2 Model 80  
OPERATING SYSTEM: MS-DOS 5.0  
SOFTWARE: Microsoft Word 5.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/754,918A

FILING DATE: 19910905

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Michaelson, Peter L.

REGISTRATION NUMBER: 30090

REFERENCE/DOCKET NUMBER: Centro-2R

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 530-6671

TELEFAX: (908) 530-6584

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1836 bp

TYPE: NUCLEOTIDE WITH CORRESPONDING AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

ORIGINAL SOURCE:

ORGANISM: N. meningitidis group B

IMMEDIATE SOURCE: Strain B:4:P1:15 isolated in Cuba

FEATURE: From 1 to 1830 bp mature protein

OTHER INFORMATION:

OTHER INFORMATION: Properties: Gene coding for P64k protein from outer membrane

US-07-754-918A-1

Query Match 57.1%; Score 12; DB 1; Length 1836;  
Best Local Similarity 100.0%; Pred. No. 97;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGACGCTT 12  
|||||

Db 449 TCGTCGACGCTT 460

## RESULT 67

US-09-555-000-1

Sequence 1, Application US/09555000

Patent No. 6489108

GENERAL INFORMATION:

APPLICANT: Genencor International, Inc.

TITLE OF INVENTION: Proteases from Gram Positive Organisms

FILE REFERENCE: GC390-PCT

CURRENT APPLICATION NUMBER: US/09/555,000

CURRENT FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: PCT/US98/26971

PRIOR FILING DATE: 1998-12-17

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1

LENGTH: 1900

TYPE: DNA

ORGANISM: Bacillus subtilis

FEATURE:

NAME/KEY: CDS

LOCATION: (134)...(1774)

US-09-555-000-1

Query Match 57.1%; Score 12; DB 4; Length 1900;  
Best Local Similarity 100.0%; Pred. No. 97;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GTCGACGCTTCG 14  
|||||

Db 1108 GTCGACGCTTCG 1119

## RESULT 68

US-08-358-117-1/c

Sequence 1, Application US/08358117

Patent No. 5608147

GENERAL INFORMATION:

APPLICANT: Kaphammer, Bryan J.

TITLE OF INVENTION: ttda Gene Selectable Markers in Plants and the

TITLE OF INVENTION: Use Thereof

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESS: Stearns, Kessler, Goldstein &amp; Fox

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/358,117

FILING DATE: 15-DEC-1994

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1405.0030001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2058 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 751...1611

US-08-358-117-1

Qy 8 ACCTTCGAGATG 19  
|||||

Db 1016 ACCTTCGAGATG 1005

## RESULT 69

US-08-470-588-1/c

Sequence 1, Application US/08470588

Patent No. 6100446

GENERAL INFORMATION:

APPLICANT: STREIBER, WOLFGANG R.

APPLICANT: TIMMIS, KENNETH N.

APPLICANT: ZENK, WEINHART H.

TITLE OF INVENTION: MICROORGANISMS AND PLASMIDS FOR

TITLE OF INVENTION: 2,4-DICHLOROPHENOXACETIC ACID (2,4-D) MONOOXYGENASE

TITLE OF INVENTION: FORMATION AND PROCESS FOR THE PRODUCTION OF THESE PLASMIDS

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESS: FROMMER LAWRENCE &amp; HAUG LLP

STREET: 745 FIFTH AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10151  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/470.588  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: LAWRENCE, WILLIAM F.  
REGISTRATION NUMBER: 28,029  
REFERENCE/DOCKET NUMBER: 514413-3526  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-588-0800  
TELEFAX: 212-588-0500  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2058 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-470-588-1

Query Match  
Best Local Similarity 100.0%; Score 12; DB 3; Length 2058;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACGTTCGAGATG 19  
|||||  
Db 1016 ACGTTCGAGATG 1005

RESULT 70  
US-08-528-026C-3/C  
Sequence 3, Application US/08528026C  
Patent No. 6248566  
GENERAL INFORMATION:  
APPLICANT: IMANAKA, Tadayuki  
APPLICANT: TERADA, Yoshinobu  
APPLICANT: TAKAHARA, Takeshi  
APPLICANT: YANASE, Michio  
APPLICANT: OKADA, Shigetaka  
APPLICANT: TAKATA, Hiroki  
APPLICANT: NAKAMURA, Hiroyasu  
APPLICANT: FUJII, Kazutoshi  
TITLE OF INVENTION: GLUCAN HAVING CYCLIC STRUCTURE AND METHOD FOR PRODUCING THE SAME  
FILE REFERENCE: 9900-0002.20  
CURRENT APPLICATION NUMBER: US/08/528,026C  
PRIOR FILING DATE: 1995-09-13  
PRIOR APPLICATION NUMBER: US 08/445,152  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: Patentin Version 3.0  
SEQ ID NO: 3  
LENGTH: 2426  
TYPE: DNA  
ORGANISM: Bacillus stearothermophilus (Strain TRBE14)  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (385) (392)  
OTHER INFORMATION: S SD sequence  
NAME/KEY: misc\_feature  
LOCATION: (402) (2357)  
OTHER INFORMATION: P CDS  
US-08-528-026C-3

Query Match  
Best Local Similarity 100.0%; Score 12; DB 3; Length 2426;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CGTTCGAGATGA 20  
|||||  
Db 1278 CGTTCGAGATGA 1267

RESULT 71  
US-09-221-017B-225  
Sequence 225, Application US/09221017B  
Patent No. 6444799  
GENERAL INFORMATION:  
APPLICANT: ROSE, Bruce C.  
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF  
NUMBER OF SEQUENCES: 1120  
CORRESPONDENCE ADDRESS:  
ADDRESSER: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/221,017B  
FILING DATE: 23-DEC-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PP1182  
FILING DATE: 31-DEC-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PP1546  
FILING DATE: 30-JAN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PP2911  
FILING DATE: 09-APR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/AU98/01023  
FILING DATE: 10-DEC-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Monroy, Gladys H  
REGISTRATION NUMBER: 32,430  
REFERENCE/DOCKET NUMBER: 27340-20021.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-813-5600  
TELEFAX: 650-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 225:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2572 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: UNKNOWN  
ORIGINAL SOURCE:  
ORGANISM: PORPHYROMONAS GINGIVALIS  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1...2572  
US-09-221-017B-225

Query Match  
Best Local Similarity 100.0%; Score 12; DB 4; Length 2572;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCGAGATGAT 21  
|||||  
Db 936 GTTCGAGATGAT 947

## RESULT 72

US-09-619-353-13  
Sequence 13, Application US/09619353  
Patent No. 6410249  
GENERAL INFORMATION:  
APPLICANT: Ngai, John  
APPLICANT: Specia, David J.  
APPLICANT: Lin, David M.  
APPLICANT: Isaacoff, Erud Y.  
APPLICANT: Diltman, Andrew H.  
APPLICANT: Fan, Jinhong  
TITLE OF INVENTION: Odorant Receptors  
FILE REFERENCE: B99-038-2  
CURRENT APPLICATION NUMBER: US/09/619,353  
CURRENT FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: 60/144,766  
PRIOR FILING DATE: 1999-07-20  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 13  
LENGTH: 2595  
TYPE: DNA  
ORGANISM: Brachydanio rerio (zebrafish)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (4)..(2592)  
US-09-619-353-13

Query Match 57.1%; Score 12; DB 4; Length 2595;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGTTCGAGATGA 20  
|||||  
Db 1964 CGTTCGAGATGA 1975

## RESULT 73

US-09-221-017B-462/C  
Sequence 462, Application US/09221017B  
Patent No. 6444799  
GENERAL INFORMATION:  
APPLICANT: Ross, Bruce C.  
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF  
NUMBER OF SEQUENCES: 1120  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FORSTER  
STREET: 755 PAGE MILL ROAD  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/221,017B  
FILING DATE: 23-DEC-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PP1182  
FILING DATE: 31-DEC-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PP1546  
FILING DATE: 30-JAN-1998  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PP2811  
FILING DATE: 09-APR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/AU98/01023  
FILING DATE: 10-DEC-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: MONROY, Gladys H  
REGISTRATION NUMBER: 32,430  
REFERENCE/DOCKET NUMBER: 27340-20021.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-813-5600  
TELEFAX: 650-494-0792  
TELEX: 706141

INFORMATION FOR SEQ ID NO: 462:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2760 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: UNKNOWN  
ORIGINAL SOURCE:  
ORGANISM: PORPHYROMONAS GINGIVALIS  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1...2760  
US-09-221-017B-462

Query Match 57.1%; Score 12; DB 4; Length 2760;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ACGTTCGAGATG 19  
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Db 2296 ACGTTCGAGATG 2285

## RESULT 74

US-09-252-991A-3523  
Sequence 3523, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 3523  
LENGTH: 2832  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-3523

Query Match 57.1%; Score 12; DB 4; Length 2832;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGTTCGAGATGA 20  
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Db 1490 CGTTCGAGATGA 1501

## RESULT 75

US-08-936-165A-66/C  
Sequence 66, Application US/08936165A  
Patent No. 6348582

GENERAL INFORMATION:  
APPLICANT: Black, Michael  
APPLICANT: Burnham, Martin  
APPLICANT: Hodgson, John  
APPLICANT: Knowles, David  
APPLICANT: Lonetto, Michael  
APPLICANT: Nicholas, Richard  
APPLICANT: Pratt, Julie  
APPLICANT: Reichard, Richard  
APPLICANT: Rosenbery, Martin  
APPLICANT: Ward, Judith  
TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,  
TITLE OF INVENTION: Polypeptides and Their Uses  
NUMBER OF SEQUENCES: 534  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/936,165A  
FILING DATE: 24-SEP-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/027,032  
FILING DATE: 24-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Gimm, Edward R  
REGISTRATION NUMBER: 38, 891  
REFERENCE/DOCKET NUMBER: P50549  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2854 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
US-08-936-165A-66

Query Match 57.1%; Score 12; DB 4; Length 2854;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGTTCGAGATGA 20  
|||||  
Db 1984 CGTTCGAGATGA 1973

Search completed: December 17, 2003, 10:01:51  
Job time : 67 secs

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